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Dysregulated antibody, natural killer cell and immune mediator profiles in autoimmune thyroid diseases

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Abstract: The pathogenesis of autoimmune thyroid diseases (AITD) is poorly understood and the association between different immune features and the germline variants involved in AITD are yet unclear. We previously observed systemic depletion of IgG core fucosylation and antennary α1,2 fucosylation in peripheral blood mononuclear cells in AITD, correlated with anti-thyroid peroxidase antibody (TPOAb) levels. Fucose depletion is known to potentiate strong antibody-mediated NK cell activation and enhanced target antigen-expressing cell killing. In autoimmunity, this may translate to autoantibody-mediated immune cell recruitment and attack of

self-antigen expressing normal tissues. Hence, we investigated the crosstalk between immune cell traits, secreted proteins, genetic variants and the glycosylation patterns of serum IgG, in a multi-omic and cross-sectional study of 622 individuals from the TwinsUK cohort, 172 of whom were diagnosed with AITD. We observed associations between two genetic variants (rs505922 and rs687621), AITD status, the secretion of Desmoglein-2 protein, and the profile of two IgG N-glycan traits in AITD, but further studies need to be performed to better understand their crosstalk in AITD. On the other side, enhanced afucosylated IgG was positively associated with activatory CD335-CD314+CD158b+ NK cell subsets. Increased levels of the apoptosis and inflammation markers Caspase-2 and Interleukin-1α positively associated with AITD. Two genetic variants associated with AITD, rs1521 and rs3094228, were also associated with altered expression of the thyrocyte-expressed ligands known to recognize the NK cell immunoreceptors CD314 and CD158b. Our analyses reveal a combination of heightened Fc-active IgG antibodies, effector cells, cytokines and apoptotic signals in AITD, and AITD genetic variants associated with altered expression of thyrocyte-expressed ligands to NK cell immunoreceptors. Together, TPOAb responses, dysregulated immune features, germline variants associated with immunoactivity profiles, are consistent with a positive autoreactive antibody-dependent NK cell-mediated immune response likely drawn to the thyroid gland in AITD.

Keywords: Multi-omic; autoimmune thyroid diseases (AITD); genetic variants; apoptosis; antibody-dependent cell-mediated cytotoxicity (ADCC); anti-thyroid peroxidase antibody (TPOAb)

1. Introduction

Autoimmune thyroid diseases (AITD) are a class of chronic, organ-specific disorders of the thyroid gland with a high genetic heritability (55-75%) [1–4] affecting approximately 5% of the population and with a gender disparity (i.e., women: 5-15%; men: 1-5%) [5–7]. Pathologically, AITD are characterized by autoantibodies against three main thyroid proteins (thyroid peroxidase (TPO), thyroglobulin (Tg), and the thyroid-stimulating hormone (TSH) receptor (TSH-R)), infiltration of the thyroid gland by immune cells (e.g. lymphocytes, NK cells, monocytes, and macrophages), the formation of germinal centers in the thyroid gland [8] and dysregulated TSH levels [9,10]. However, some studies have failed to observe a significant difference in peripheral blood immune cell composition between AITD patients and healthy individuals [11], while others report significant differences in particular cell types or in immune marker expression [12]. Immune cells, thyroid autoantibodies, and secreted proteins including cytokines may play critical roles in AITD development [13] and in immune responses, including in antibody-dependent cell-mediated cytotoxicity (ADCC) pathways [14,15]. However, the underlying autoimmune signatures associated with AITD remain unclear.

ADCC is triggered via antigen/antibody/Fc receptor complex formation, bringing the effector cell (macrophages, NK cells) and the target cell (expressing the antigen) in close contact. The formation and function of antigen/antibody complexes are modulated by various factors including post-translational modifications of glycans decorating antibodies [16,17]. One example is lack of fucose on the N-linked core glycan of IgG. Afucosylated antibodies have a higher affinity (~100-fold) for the immunoglobulin Fc receptor FcγRIIIa (CD16a), expressed on NK cells, macrophages and $\gamma\delta$ T cells, and are shown to confer enhanced ADCC potential *in vitro* and anti-tumor activity *in vivo* [18–21]. This could result in antibodies with more potent Fc-mediated effector functions able to more effectively recruit and activate immune effector cells such as NK cells to kill target antigen-expressing cells [22,23]. IgG core fucose, observed in approximately 95% of IgG in healthy individuals, is considered a "safe switch" that can attenuate potentially harmful antibody-dependent damage against self-antigen-expressing normal tissues [18–21,24]. However, it is possible that these processes may be altered in autoimmune diseases.

We previously studied the glycosylation profiles of total immunoglobulin G (IgG) and of peripheral blood mononuclear cells (PBMC) in patients with AITD [4], as well as the glycosylation of IgG-depleted serum proteins in Hashimoto's thyroiditis (HT) patients [25]. In peripheral blood, we identified both depleted core fucosylation of IgG antibodies and decreased antennary α1,2 fucosylation of PBMC to be associated with autoantibodies to thyroid peroxidase (TPOAb) and AITD status [4]. We also identified a network of genes, including *FUT8* and *IKZF1* that regulate fucosylation, to be implicated in the development of AITD [4,26]. Based on these findings, we speculated that IgG core fucose deficiencies together with elevated levels of autoantibodies may participate in autoimmune responses in AITD by enhancing effector cell activation and heightened immune and inflammatory signals.

Therefore, here we investigated immune features that may signify dysregulated, and likely heightened immune effector cells, antibodies, and immune mediators in AITD. In this *in silico* study in the blood of 622 subjects from the TwinsUK cohort, of whom 172 have AITD features, we aimed to investigate: 1) the association of different components of antigen/antibody/Fc receptor complexes with AITD; 2) the associations between these different immune components in a cohort of samples from volunteers regardless of disease status, and 3) potential genetic drivers on these components (study design summarized in **Fig. 1**). Specifically, we examined the association of total serum IgG glycosylation, immune traits, such as immune cell subpopulation frequencies (CSFs; i.e. relative frequencies of circulating immune cell subsets), immune cell surface protein expression levels (SPELs; i.e. the measurement of the cell-surface expression of critical proteins) and secreted proteins, in the peripheral blood of patients with AITD compared with those of healthy volunteers (sample sizes of each study performed are summarized in **Table S1**).

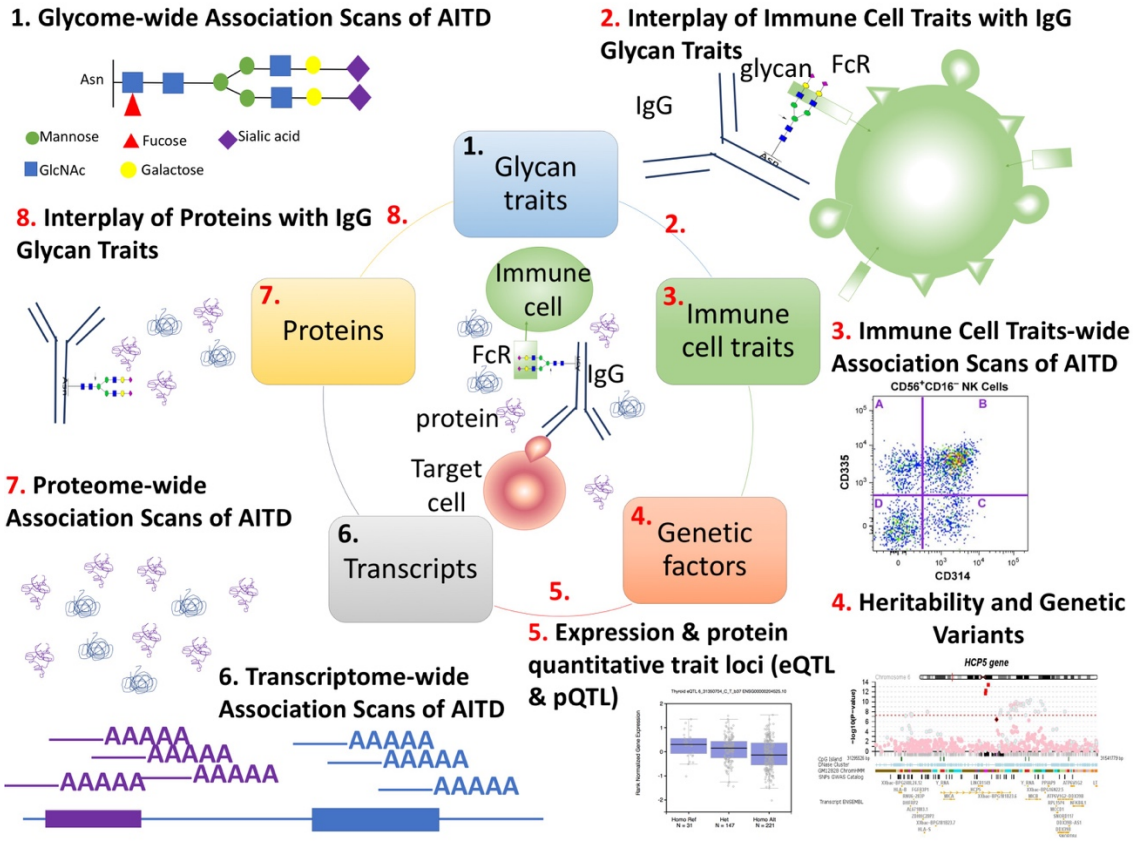

Figure 1. Multi-omics computational analyses were used to study the components of antigen/antibody/effector cell complex structure in AITD. 1) We previously performed glycome-wide association studies of AITD and TPOAb levels using 3,146 individuals from three European cohorts, including the TwinsUK cohort. We identified 17 AITD-IgG N-glycan traits in the discovery TwinsUK cohort, and seven of these 17 have been then replicated in two other cohorts [4]. 2) In the present

study, we studied the association of total IgG N-glycan traits with 23,485 immune cell traits in 383 individuals from the TwinsUK cohort (regardless of disease status). We showed that 6 out of the 17 AITD-IgG glycan traits were correlated with 51 immune cell traits featuring the CD335, CD134, and CD158b receptors. 3) None of these 51 immune cell traits appeared to be associated with AITD in 374 individuals (34 with AITD). 4) The heritability of AITD, TPOAb level and several -*omic* features (IgG N-glycan traits and immune cell traits) were performed in previous studies of the TwinsUK cohort [4,27–29]. Here we estimated the heritability of secreted proteins, but we could not determine shared additive genetic variance between different phenotypes studied (AITD status, TPOAb level, level of IgG N-glycan traits, of immune cell traits and of circulating proteins in the bloodstream). 5) We identified genetic variants that alter the expression of genes, proteins and cell-bound immune receptors (highlighted in this study) using the previous GWASs performed in the TwinsUK cohort or from GWAS catalog, eQTLs from GTEx project and pQTLs from INTERVAL project [27,28,30–35]. 6) We previously performed transcriptome-wide association studies of AITD, TPOAb level, and N-glycan structures in the whole blood of approximately 300 individuals and we found no significant associations [4]. 7) We observed 3 out of 1,113 circulating proteins tested in plasma of almost 300 individuals shown to be associated with AITD status (TSH, Caspase-2, and Interleukin-1α). 8) Several secreted proteins were correlated with the level of plasma IgG glycan traits in 164 individuals, but none of them were also associated with AITD. The sample sizes of these different studies are described in **Table S1**. GlcNAc = N-acetylglucosamine. The numbers in black depict analyses performed previously [4,27–29] while the numbers in red depict analyses presented for the first time in the present study.

2. Materials and Methods

2.1. Study Sample

The study was conducted using immune cell traits, glycosylation, proteomics, genotyping, and phenotypes in samples from research volunteers from the UK Adult Twin Registry (TwinsUK cohort). The TwinsUK cohort is comprised of approximately 14,000 monozygotic and dizygotic same-sex adult twins from the UK, unselected for any particular disease or trait (**Table S1)**. The cohort is of Northern European/UK ancestry and has been shown to be representative of singleton populations and the UK population in general [36,37]. Ethical approval was granted by the National Research Ethics Service London-Westminster, the St Thomas' Hospital Research Ethics Committee (EC04/015 and 07/H0802/84). Informed consent was obtained from all study participants.

2.2. Data Statement

Multi-omic data were derived from samples in the TwinsUK cohort. Individual-level TwinsUK data, including phenotypes and genotypes, are not permitted to be shared or deposited due to the original consent given at the time of data collection. Access data can be applied for through the TwinsUK data access committee (http://twinsuk.ac.uk/resources-for-researchers/access-our-data/).

2.3. Definition of AITD and detection of TSH and TPOAb

The study was performed using a clinical AITD definition and TPOAb as a threshold trait; it was not possible for AITD (Hashimoto's disease and Graves' disease) clinical diagnosis to be confirmed by a clinician. However, approximately 90% of individuals with Hashimoto's disease, about 75% with Graves' disease, <20% with other thyroid diseases, and <10% of normal individuals are known to have TPOAb-positivity [38–40]. Therefore, individuals were considered to have AITD if they either showed significantly higher than normal TPOAb serum titers (set at 3-fold higher than the threshold set by the manufacturer [18 IU/mL for the Abbott assay and 100 IU/mL for the Roche assay]) or had TSH serum levels >10 mIU/L. We considered individuals as controls if they had normal levels of TSH and a negative TPOAb titer, with no previous clinical diagnosis of thyroid disease and who were not treated with thyroid medications or steroids. Individuals with a history of thyroid cancer or thyroid surgery were excluded. Among the 622 individuals studied, 172 (27.65%) were

identified with AITD, 236 (37.94%) considered normal controls, and 214 (34.41%) have TPOAb or TSH serum levels outside the normal range, but do not reach the 3-fold cutoff for inclusion in the AITD cohort. Evaluations of sera to measure TPOAb and TSH levels are described in **Appendix A**.

2.4. Detection of IgG glycosylation profiling for discovery

Plasma specimens for analysis of IgG glycosylation was collected between 1997 and 2013 in 2,279 individuals from the TwinsUK cohort. IgG glycosylation profiling was performed on total plasma IgGs glycome (combined Fc and Fab glycans and all IgG subclasses) in Genos Glycoscience Research Laboratory, Croatia using UPLC analysis of 2AB-labelled glycans. Protocol, data pre-processing and normalization in the TwinsUK cohort were previously described [4] (**Appendix A**).

2.5. Detection of immune cell traits

Plasma samples for assessment of 78,000 immune traits were collected between 2010 and 2012 in 669 female participants from the TwinsUK cohort using high-resolution deep immunophenotyping flow cytometry analysis as previously described [28]. 78,000 different cell surface marker combinations captured by 7 distinct 14-color immunophenotyping panels were detected and described immune cell subset frequencies (CSF) and immune cell-surface protein expression levels (SPELs). After quality control to remove immune cell traits that appeared as poor reproducibility or out of range, 23,485 immune cell traits from 497 individuals of the TwinsUK cohort were analyzed. For this analysis, only 374 twins had immune cell traits data and TPOAb level detected by Roche immunoassay and 245 individuals in a case-control study by combining Roche and Abbott assays (204 controls and 41 AITD). Immune traits were quantile normalized residuals of a linear mixed effect model where age was included as fixed effects, and the batches were considered as random effects.

2.6. Detection of protein profiling in plasma

With an aptamer-based multiplex protein assay (SOMAscan v2, SomaLogic Inc, Boulder, CO) [41,42], 1,129 proteins were measured (2013) on plasma samples collected between 2004 and 2011 from 211 female twins of the TwinsUK cohort (**Appendix A**).

2.7. Statistical analyses

All statistical analyses were run using R version 3.2.3. Linear mixed effect models were conducted using the R lme of package lme4 [43], and linear models were done in using R function lm of package stat. Custom R scripts developed for this study are available at this URL: https://github.com/TiphaineCMartin/multiomic_AITD.git.

For determination of effective number of independent tests for different *-omic* data, association studies between *-omics* features and thyroid phenotypes and heritability analysis for proteins (**Appendix A)**.

2.8. Genome-wide Association Analysis on IgG N-glycan traits

To define genetic variants (i.e., single nucleotide polymorphisms (SNP), short insertions and deletions (indels)) associated with glycosylation profiles regardless of specific phenotypes in the TwinsUK cohort, we ran analyses with the GenABEL software package [44] designed for genome-wide association study (GWAS) analysis of family-based data by incorporating pairwise kinship matrix calculated using genotyping data in the polygenic model to correct relatedness and hidden population stratification. Data were recently published with other datasets [26,45]. We selected genetic variants for each IgG N-glycan traits with a P-value under the GWAS threshold (P-value < $5x10^{-8}$) and added the list of previously-defined genetic variants [29,45] (**Appendix A**).

2.9. Determination of shared genetic variants and genes between IgG N-glycan traits, immune cell traits, protein abundance, and thyroid functions and diseases

To examine whether IgG N-glycan, immune cell traits, proteins, thyroid functions and diseases shared genetic variants or genes, we compared the genetic variants from GWASs on TwinsUK data (NHGRI GWAS catalog and other projects). As genetic variants detected by GWASs could be lead genetic variants but not necessarily causal genetic variants [46], we extended the list of genetic variants to other variants in linkage disequilibrium (LD) with an r^2 threshold of 0.8 from 1000G Phase 1 European population. Using HaploReg V4.1 [47] and GTeX data [32,33], we extracted tissue-specific expression quantitative traits (eQTLs) associated with these genetic variants.

2.10. Visualization

Heatmaps were created in using R package ComplexHeatmap. Correlation plots were created with R package corrplot. Boxplots and scatter plot were created in using R package ggplot2.

3. Results

3.1. Depletion of IgG core fucose is positively associated with increased CD158b+CD314+CD335- NK cell subset counts

IgG N-glycosylation is considered indispensable for the effector functions of IgG and inflammation control [48–52] and plays an essential role in the recognition and binding to Fc receptors of immune cells [51]. Using high-resolution deep immunophenotyping flow cytometry analysis in 669 twins from the TwinsUK cohort and IgG N-Glycan traits in 2,297 twins from the same cohort [4,27,28], we identified 383 samples with measurements of 23,485 immune cell and 17 AITD-IgG N-glycan traits (IGP2, IGP7, IGP8, IGP15, IGP21, IGP33, IGP36, IGP42, IGP45, IGP46, IGP48, IGP56, IGP58, IGP59, IGP60, IGP62 and IGP63) and searched for any associations between them (**Table S1**).

In our cohort, we identified 1,357 independent immune cell traits among 23,485 potential tested immune cell traits, where the partial correlation between immune cell traits is highlighted in **Fig. S1a**, 20 independent IgG N-glycan traits among 75 potential tested IgG N-glycan traits, and 6 independent AITD-IgG N-glycan traits among 17 potential tested AITD-IgG N-glycan traits [53]. Association studies of total IgG N-glycan traits with immune cell traits showed that 6 of the 17 identified significant IgG N-glycan traits (IGP2, IGP42, IGP46, IGP58, IGP59, IGP60) previously associated with TPOAb level and AITD status in the TwinsUK cohort, were also associated with 51 immune cell traits, which are all NK cells (CD16+CD56) featuring different combinations of 6 immunoreceptors (CD2, CD158a, CD158b, CD314, CD335, R7) (**Table S2, Fig. 2**). Three IgG N-glycan traits without core fucose (IGP2, IGP42, IGP46) were negatively associated with the level of the activating subpopulation of $CD16^+CD56^+CD158b^-CD335^+$ NK cells and positively associated with the level of the $CD16^+CD56^+CD335^-$ effector NK cell subpopulation and with the activating subpopulation $CD16^+CD56^+CD158b^+CD314^+CD335^-$ NK cells [54–59]. In contrast, three other significant IgG N-glycan traits with core fucose (IGP58, IGP59, and IGP60) had the opposite effect associations with the same subpopulations of NK cells (**Fig. 2a)**. In agreement with our previous report, there are therefore negative correlations between the set of IgG N-glycan traits without core fucose (IGP2, IGP42, IGP46) and the set of IgG N-glycan traits describing IgG core fucose (IGP58, IGP59, and IGP60) [4] (highlighted in **Fig. 2b)**. Moreover, we observed strong correlations between these 51 immune cell traits (**Fig. 2c**). The presence of correlation patterns between the 17 AITD-IgG N-glycan traits (**Fig. 2b**) as well as between the 51 immune cell traits (**Fig. 2c**) is consistent with our observation of correlations between the 6 AITD-IgG N-glycan traits and the 51 immune cell traits **(Fig. 2a)**. When we extended our analysis to the 58 remaining IgG N-glycan traits also identified in our samples, but not associated with AITD, we observed no significant association between them and the 23,485 immune cell traits. Moreover, for 23,485 peripheral blood immune cell traits (**Table S1**), no significant association with AITD or TPOAb level could be identified (**Fig. S1b**).

We conclude that a subpopulation of NK cells (CD16+CD56) and specifically the activating subpopulation $CD16^+CD56^+CD158b^+CD314^+CD335^-$ NK cells is associated with fucose-depleted IgG in individuals with AITD.

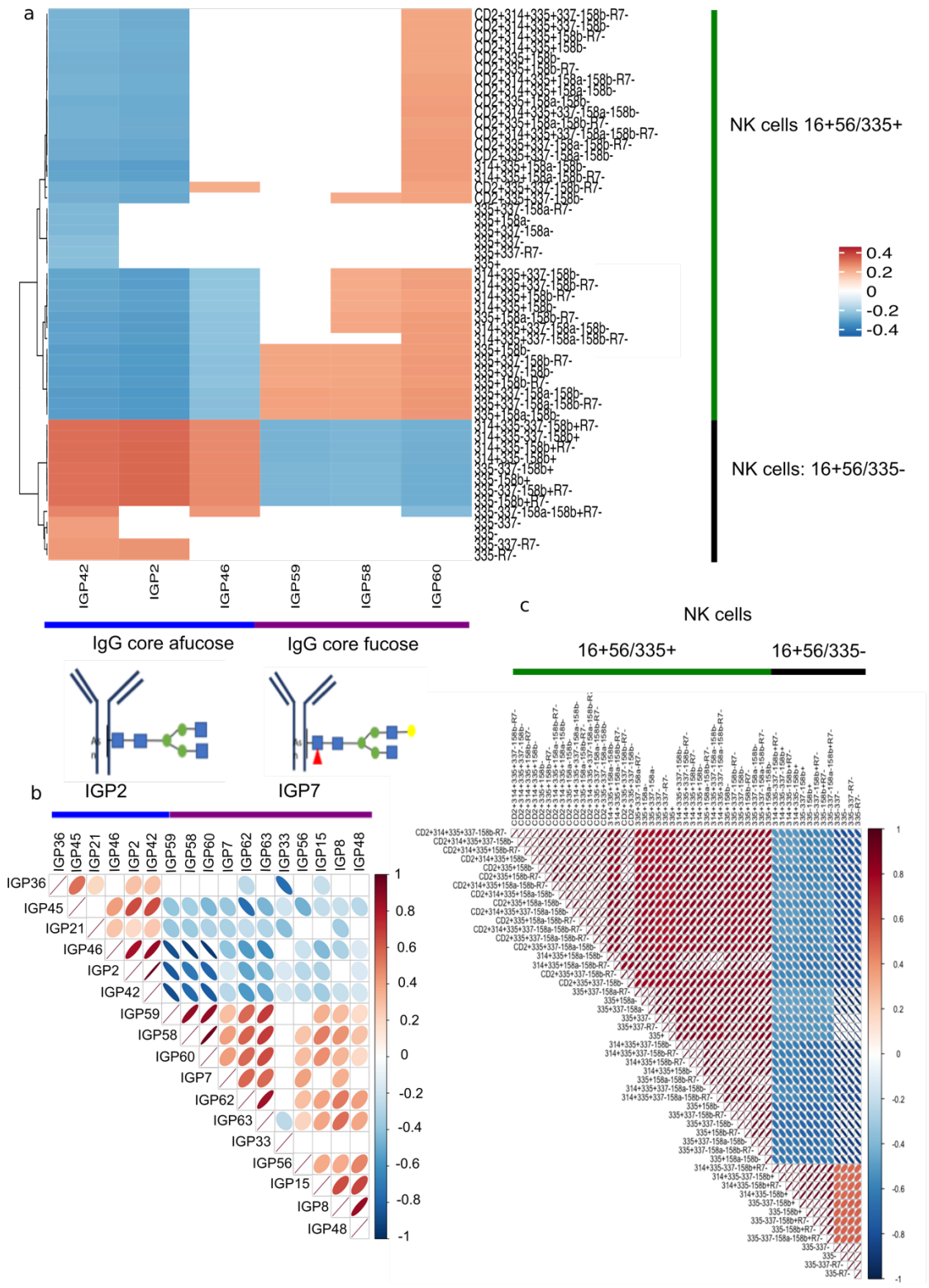

Figure 2. AITD-IgG N-glycan traits associated with a subpopulation of NK cells. (a) Heatmap of immune cell traits associated with AITD-IgG N-glycan traits. The 51 NK cell types were significantly associated with 6 out of 17 AITD-IgG N-glycan traits previously identified [4]. Below the heatmap, there are one representative of IgG core afucose (IGP2) and one representative of IgG core fucose (IGP7), that were both associated with AITD and TPOAb levels [4]. (b) Co-expressions between only 17 IgG N-glycan traits previously associated significantly with AITD status and TPOAb level [4]. (c)

Correlations between the profile of 51 immune cell traits that were associated significantly with at least one of 17 AITD-IgG N-glycan traits. The order of immune cell traits is the same as that in Fig 2a.

3.2. The AITD-associated genetic variants, rs1521 and rs3094228, alter thyroid cell expression of ligands for CD314 and CD158b immunoreceptors

The NK cell receptors, CD335 (NKp46), CD314 (NKG2D*)* and the killer cell immunoglobulin-like receptors (KIRs) including CD158b, are normally associated with activated NK cell states, T cell co-stimulation, and mediating tumor cell lysis [55,57]. To determine whether genetic factors could contribute to AITD, related immune features, or their pathways, we inspected genetic variants associated with AITD, TPOAb levels, and immune cell traits from previous GWAS [27,28,30]. We then compared these with recent large-scale studies on tissue-specific expression quantitative traits (eQTLs) [35], mainly from the GTEx project [32–34] in blood and thyroid tissue.

No genetic variants previously associated with AITD or other thyroid phenotypes appeared to be associated with the expression of CD335 or its known ligands in blood and thyroid cells. However, we observed that two genetic variants, rs1521 and rs3094228, associated with Graves' disease and TPOAb-positivity, respectively, fall in the gene regulatory regions of *MIC-A* and *MIC-B* genes, two ligands of CD314 (NKG2D), and alter their gene expressions in thyroid cells [32–34,60–62] (**Fig. 3, Table S4, Fig. S2**). These two AITD-genetic variants, rs1521 and rs3094228, also alter the expression of the *HLA-C* gene, ligand of CD158b, in thyroid cells. The Graves' disease (GD) risk allele of rs1521 variant is primary associated with a reduced expression of *HLA-C* gene, ligand of CD158b, in thyroid cells. Furthermore, the TPOAb-positivity risk allele of rs3094228 variant is primary associated with an increased expression of *MIC-B* gene, ligand of CD314 (NKG2D), in thyroid cells. As about 75% of patients with Graves' disease have TPOAb-positivity and rs3094228 that has been associated with TPOAb-positivity and Graves' disease [61,63], it is possible that the association of rs1521 with Graves' disease could be also driven by TPOAb-positivity and, so, associated with its phenotypes. Downregulation of *HLA-C* gene expression and upregulation of *MIC-A* and *MIC-B* gene expression in thyrocytes could activate NK cell functions and the cytokine production against thyrocytes when NK cells and thyrocytes are in contact.

Furthermore, three genetic variants, rs2596460, rs2596457 and rs2523691, previously associated with higher levels of the subpopulation of NK cells featuring $CD16^{+}CD56/CD2^{-}CD314^{+}CD335^{-}CD337^{-}CD158a^{+}CD158b^{+}$ [28], are in the same haplotype as the rs3094228 genetic variant, but with a low linkage disequilibrium (LD, $r^2 < 0.8$) (**Table S5)**. Potentially, one of the genetic variants in this locus are the causal genetic variant of higher abundance of $CD158b^{+}CD314^{+}CD335^{-}$ NK cells. All of the three genetic variants could also alter the expression of the *HLA-C* gene, ligand of CD158b, and *MIC-A*, ligand of CD314 (NKG2D), in immune cells [32–34,64] (**Fig. 3, Table S4**).

Overall, two genetic variants, rs1521 and rs3094228, associated with, respectively, Graves' disease and TPOAb-positivity, appear to alter thyrocyte expression of ligands of two immunoreceptors of NK cells, CD314 and CD158b; both of which have the capacity to enhance cytotoxicity of NK cells after binding with target cells. Additionally, three genetic variants in the same haplotype than rs3094228 could increase the abundance of the immune active $CD158b^{+}CD314^{+}CD335^{-}$ NK cell subpopulation.

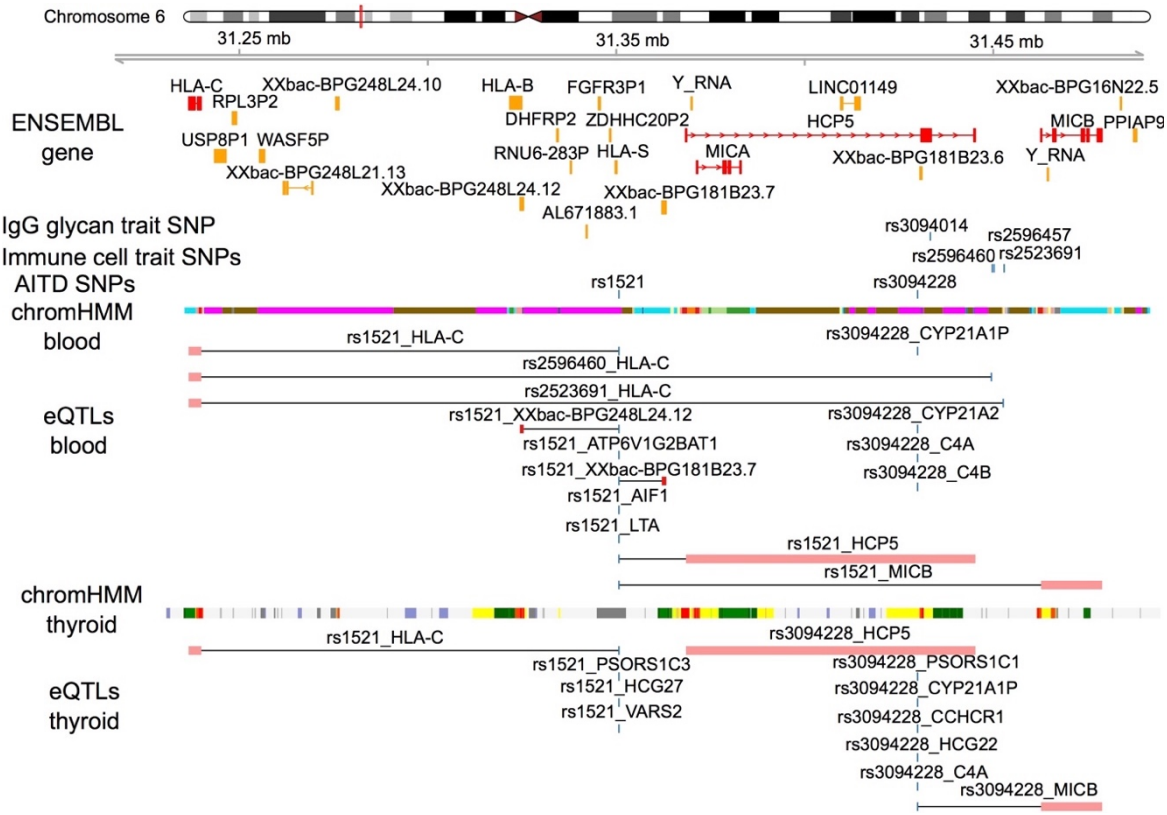

Figure 3. Association of immune cell traits with AITD status. Annotation tracks around *MIC-A, MIC-B* and *HLA-C* genes visualize significant GWAS hits for immune cell traits, the ligands of certain immunoreceptors (such as NK), and thyroid phenotypes previously identified in the TwinsUK cohort as well as chromatin states identified using chromHMM from whole blood from ENCODE [65] and thyroid cells from CEMT [66] and eQTLs from GTEx project [32,33]. The plot was produced using functions from R packages Gviz and coMET [67].

3.3. AITD is associated with increased serum Caspase-2 and IL-1α

We next evaluated whether the abundance of 1,113 free soluble proteins, which are partially correlated between each other (**Fig. 4a**), in peripheral blood may be associated with AITD status (27 AITD patients versus 130 healthy controls) and TPOAb levels (155 individuals of whom 25 have AITD) in the TwinsUK cohort (**Table S1**) using aptamer-based multiplex protein assay **(**SOMAscan) [68]. Firstly, we observed significant moderate correlations of the TSH levels measured by two clinical-certificated assays (Abbott and Roche) with the TSH levels measured by the SOMAscan assay (**Fig. 4b**). This indicated that the SOMAscan assay could reproduce with good accuracy the estimation of TSH levels and probably also for other proteins. Levels of three proteins were positively associated with AITD status (Bonferroni multiple testing correction, P-value<1.9×10^{-4}): TSH (P-value=8.67×10^{-5}; Beta=0.67; SE=0.16), Caspase-2 (CASP-2; P-value=2.72×10^{-7}; Beta=1.10; SE=0.20) and Interleukin-1α (IL-1α; P-value=7.46×10^{-5}; Beta=0.41; SE=0.09). We also observed higher mean levels of TSH in patients with AITD ($mean_{SOMAscan}$=1443.9, $sd_{SOMAscan}$=1238.5; $mean_{clinical}$=7.1 IU/mL, $sd_{clinical}$=10.47) or TPOAb-positivity ($mean_{SOMAscan}$=1389.9, $sd_{SOMAscan}$=1018.3; $mean_{clinical}$=5.7 IU/mL, $sd_{clinical}$=7.55) compared with controls (euthyroidism with TPOAb-negative) ($mean_{SOMAscan}$=851.1, $sd_{SOMAscan}$=368.6; $mean_{clinical}$=1.64 IU/mL, $sd_{clinical}$=0.79). Although Caspase-2 and IL-1α levels were associated with AITD status, Caspase-2 and IL-1α levels were not associated with TPOAb or TSH levels as continuous variables (P-value>1.9×10^{-4}). However, when participants were divided into 4 categories according to TSH and TPOAb levels (**Fig. 4c**), reflecting different clinical categories (hyperthyroidism, euthyroidism/TPOAb-negative, hypothyroidism and euthyroidism/TPOAb-positive), Caspase-2 showed significantly higher mean and variance in two groups: hypothyroidism and euthyroidism/TPOAb-positive (**Fig. 4d**). The hypothyroidism and euthyroidism/TPOAb-positivity in

this cohort potentially indicate underlying Hashimoto's thyroiditis (HT). This is because HT is the most common cause of hypothyroidism, spontaneous hypothyroidism (i.e. no previous history of thyroid ablation) is almost always caused by HT, and euthyroid individuals with TPOAb-positivity almost always have HT when studied by cytology and histopathology [69–71]. On the other hand, the variance of IL-1α was significantly larger in groups with euthyroidism/TPOAb-positive and hyperthyroidism (**Fig. 4e**), but there was no significant difference for their mean values. Hence, individuals from 4 categories have the same levels of IL-1α, but there are more inter-individual variabilities in euthyroidism/TPOAb-positive and hyperthyroidism than euthyroidism/TPOAb-negative and hypothyroidism.

In summary, we confirmed the association of the plasma TSH levels with AITD status, and we found two novel associations of plasma Caspase-2 and IL-1α with AITD status, but their secretion (mean and variance) seems to also depend on other factors associated with thyroid diseases such as the levels of TSH and TPOAb.

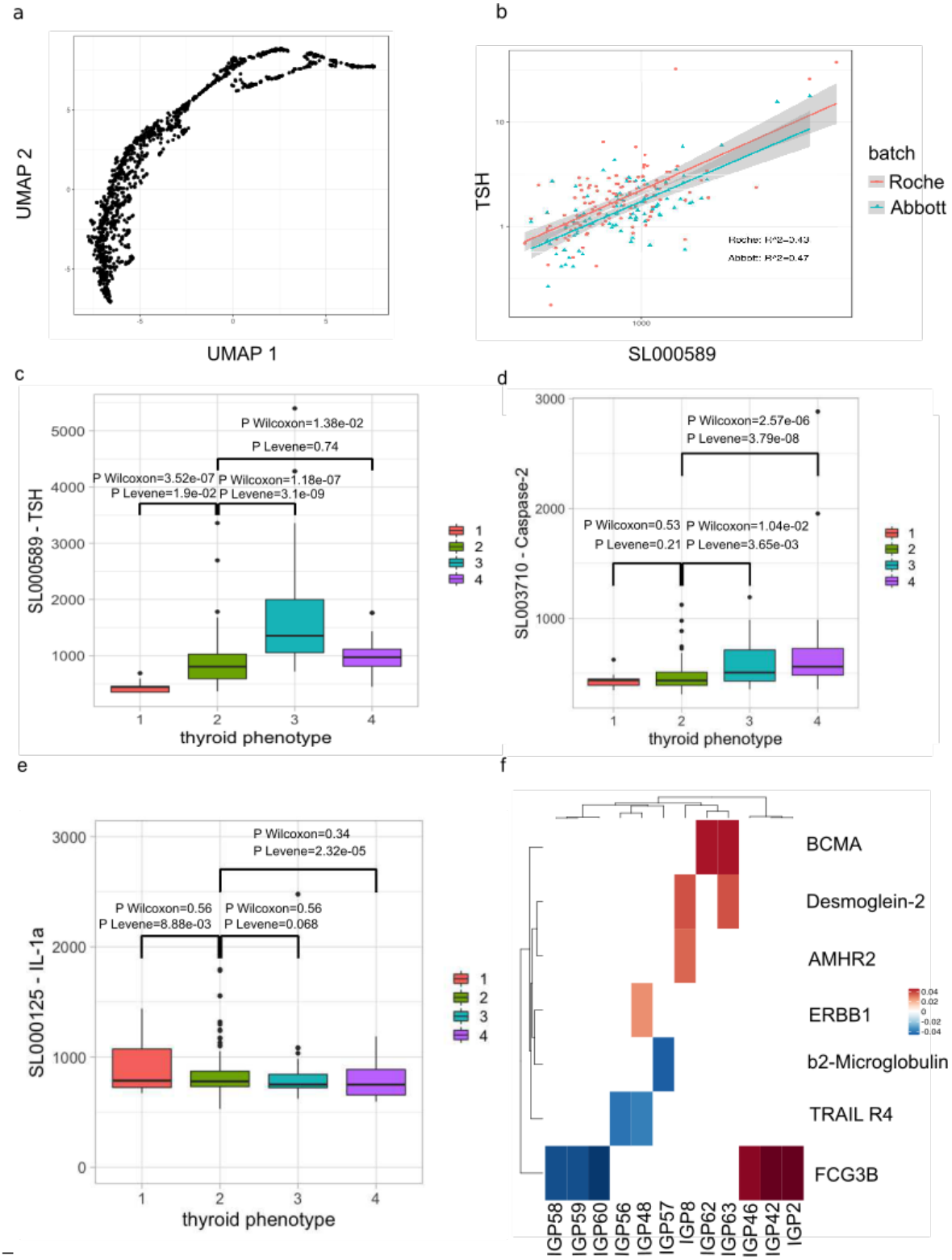

Figure 4. Association of circulating protein abundances with thyroid diseases and with AITD-IgG N-glycan structures. (a) 1,113 circulating proteins were arranged in two dimensions based on the similarity of their secretion profiles in the serum by the dimensionality reduction technique UMAP [72] using R package umapr [73]. (b) Correlation of log10-transformed TSH measurements between two clinical FDA approved clinical immunoassays (Roche and Abbott) and SOMAscan assay in 217 individuals (122 using Roche immunoassay and 95 using Abbott immunoassay). (c) Box plot of the level of circulating TSH measured by SOMAscan assay in the serum according to the group of thyroid status. (d) Box plot of the level of circulating Caspase-2 measured by SOMAscan assay in the serum according to the group of TSH. (e) Box plot of the level of circulating IL-1α measured by SOMAscan

assay. An extreme outlier sample in the group 4 with an IL-1 α of 250,000mg/ml was discarded for the analysis. (f) Heatmap of circulating protein abundances associated with AITD-IgG N-glycan structures**.** In fig.2c-e, participants were assigned to 4 categories according to TSH level and TPOAb status: 1=hyperthyroidism (TSH<=0.1 mIU/L; 13 individuals), 2=euthyroidism/TPOAb-negative (0.4<TSH>4 mIU/L & TPOAb < 6 IU/mL (Abbott) or TPOAb < 34 IU/mL (Roche); 196 healthy individuals), 3=hypothyroidism (TSH>=4 mIU/L; 21 individuals), and 4=euthyroidism/TPOAb-positive (0.4<TSH>4 mIU/L & TPOAb >= 6 IU/mL (Abbott) or TPOAb >= 34 IU/mL (Roche); 28 individuals). Wilcoxon-Mann-Whitney's test has been performed between groups to estimate whether there are mean differences whereas Levene's test has been performed between groups to estimate whether there are variance differences.

3.4. Afucosylated IgG is associated with serum levels of several circulating proteins

When we studied the correlation between the level of secreted TSH, Caspase-2 and IL-1α proteins and IgG N-glycan trait levels in 164 individuals of whom 27 have AITD, we found no significant associations (P-value>$8.3x10^{-4}$, Bonferroni test considering 3 independent proteins and 20 independent IgG N-glycan traits) (**Table S6, Fig. 4f**). However, several AITD-IgG N-glycan traits appeared to be associated with 7 other circulating proteins (AMHR2, BCMA, β2-microglobulin, ERBB1, Desmoglein-2, TRAILR4, and FCGR3B) (P-value<$3.67x10^{-5}$, Bonferroni test in considering only 227 independent proteins and 6 independent IgG N-glycan traits) (**Table S6, Fig. 4f**). For example, three AITD-IgG N-glycan traits (IGP2, IGP42, and IGP46) were positively associated with circulating FCGR3B (FcγRIIIb or CD16b), an Fc receptor expressed by polymorphonuclear neutrophils (PMN), whereas three AITD-IgG N-glycan traits (IGP58, IGP59, and IGP60) were negatively associated with the antibody Fc receptor FCGR3B. Also, IGP56 and IGP48 were negatively associated with β2-microglobulin, involved in the presentation of intracellular antigens through the MHC class I complex; and IGP48 was positively associated with ERBB1, the epidermal growth factor receptor (EGFR), a checkpoint molecule associated with cellular proliferation and differentiation.

Overall, 12 AITD-IgG N-glycan traits (IGP2, IGP8, IGP42, IGP46, IGP48, IGP56, IGP57, IGP58, IGP59, IGP60, IGP62, and IGP63) were associated with serum levels of 7 circulating proteins (AMHR2, BCMA, β2-microglobulin, ERBB1, Desmoglein-2, TRAILR4, and FCGR3B) in the TwinsUK cohort.

3.5. Free-soluble plasma Desmoglein-2 protein is associated with AITD genetic variants and two AITD-IgG N-glycan traits

We evaluated several GWAS on secreted proteins (protein quantification locus traits, pQTL) [31], to determine whether the secretion of proteins associated with AITD or with AITD-IgG N-glycan traits are driven by AITD genetic variants. We found no genetic variants associated with any of 17 AITD-IgG N-glycan structures that are also pQTL. However, four genetic variants associated with thyroid phenotypes published in the GWAS catalog (rs3761959, rs7528684, rs505922, and rs3184504) were also associated in *cis* and *trans* with nine circulating protein abundances (BGAT, CHSTB, DC-SIGN, Desmoglein-2, DYR, FCRL3, GP1BA, MBL, and VCAM-1) (**Table S7**). None of these proteins were associated directly with AITD or TPOAb levels in our study. However, we found that Desmoglein-2 was associated with two AITD-IgG N-glycan traits, IGP8, and IGP63 [4] (**Fig. S3)**. Desmoglein-2 is highly expressed in epithelial cells including thyrocytes and cardiomyocytes and plays a role in the cell-cell junctions between epithelial, myocardial, and certain other cell types and is thought to be a regulator of apoptosis [74].

Therefore, four genetic variants associated with thyroid phenotypes are also associated with nine secreted protein abundances, including the apoptosis regulator Desmoglein-2 in blood. Desmoglein-2 was also associated with two AITD-IgG N-glycan traits.

4. Discussion

The dysregulation of the immune system may affect several biological structures and processes in AITD, such as antigen/antibody/Fc receptor complex formation, possibly driven by

411 genetic and environmental factors [75]. Little is known about the key players and the genetic variants
412 identified in previous GWASs of patients with AITD. Targeting of self-antigen expressing tissues by
413 immune cells may depend on the formation of antigen/antibody/Fc receptor complexes featuring
414 substantial affinity or avidity properties. In the peripheral blood of individuals with AITD, we
415 previously detected depletion in IgG core fucose that is known to enhance such interactions and may
416 influence immune effector cell engagement of target cells by antibodies. We proposed that this
417 signature is associated with TPOAb levels and with immune effector cell activation in patients with
418 AITD [4]. Here, we reveal immune and genetic features pointing to activated NK cell subsets, thyroid
419 cell-derived ligands for immunoreceptors on NK cells, alongside secreted mediators of apoptosis and
420 immune activation, all signals of heightened antibody and innate effector cell responses in AITD.
421 We applied an *in silico* multi-omic approach on peripheral blood specimens from individuals
422 from the TwinsUK cohort to investigate any association between immune features and genetic
423 variants in AITD. In AITD patient samples, we observed increased levels of three circulating proteins
424 (TSH, Caspase-2, and Interleukin-1α) and a decreased level of IgG core fucosylation associated with
425 an activated subpopulation of NK cells defined primarily by the expression of CD335, CD134, and
426 CD158b receptors. Our data confirms the previously reported association of plasma TSH level with
427 AITD status and also reveals previously unknown potential biomarkers for AITD, which are highly
428 associated with immunological activation functions, such as ADCC, apoptosis and pro-inflammatory
429 pathways. Furthermore, several genetic variants previously associated with AITD appear to alter
430 thyrocyte gene expression of several ligands of NK immunoreceptors and abundance of plasma
431 circulating proteins. This suggest that the genetic background may also play potential roles in NK
432 cell activation likely focused on thyroid cells in individuals with AITD.
433 To our knowledge, no other cohorts have large datasets that are available to interrogate and
434 feature the same diversity of *-omics* data with AITD phenotype or TPOAb levels. In our studies, we
435 note an imbalance in the sample sizes between control individual groups and AITD groups. This is
436 because the dataset comes from unselected twins and reflects the general European population [37],
437 where approximately 5% of the population, but 5-15% for women, present individuals with AITD [5–
438 7]. To overcome such imbalances in our sample sizes and low samples sizes with large *-omics* data,
439 we applied machine learning and non-parametric methods with correction for multiple testing.
440 Another limitation in our present study is the absence of AITD clinical diagnosis confirmed by
441 clinicians for all individuals. We consequently applied more stringent criteria to define patients with
442 AITD versus control individuals, by using TSH and TPOAb levels (see Section 2.3 of our Materials &
443 Methods). We also performed analysis on TPOAb levels, as this is considered the main clinical
444 quantitative biomarker of AITD status [38–40]. Replication and meta-analysis studies on larger *-omic*
445 datasets incorporating clinical features will help to confirm our present findings.
446 Two secreted proteins (Caspase-2 and IL-1α), which play roles in apoptosis and the
447 inflammatory response, were positively associated with AITD. TPOAb have been proposed to target
448 thyroid cells by engaging effector cells via their Fc receptors [4,14,15,76,77], and the apoptosis protein
449 Caspase-2 may represent a marker potentially signifying antibody-mediated destruction of thyroid
450 cells [78]. In concordance, IL-1α, produced by activated immune, epithelial and endothelial cells in
451 response to cell injury and apoptosis, is considered an apoptosis index of the target cell [79] and
452 proportional to the degree of lymphoid infiltration in thyroid disorders [80]. IL-1α seems to reduce
453 the thyroid epithelial barrier, even in the absence of any other signs of cytotoxicity [81]. In
454 concordance, in our study we found higher levels of secreted IL-1α in AITD blood compared with
455 levels in healthy individuals, and its variance was greater in euthyroidism/TPOAb-positive blood
456 and in hyperthyroidism. This may signify dysregulation in cellular structures in the thyroid gland.
457 Overall, Caspase-2 and IL-1α may reflect the degree of thyroid cell death or apoptosis and of
458 lymphoid infiltration towards the thyroid gland.
459 A subpopulation of NK cells expressing combinations of immunoreceptors (CD2, CD158a,
460 CD158b, CD314, CD335, R7) was associated with the depletion of IgG core fucose in individuals with
461 AITD. These included an activating NK receptor (CD314) and a differentiation receptor (CD335);
462 whilst, fucose-depleted IgG was also positively associated with a subpopulation of NK cells with an

463 inhibitory NK receptor (CD158b) [54–59,82]. The combination of potentially autoreactive antibodies
464 with enhanced Fc domains and activated effector cells such as NK cells may signal increased
465 inflammation and susceptibility to autoimmune disease [83]. Previous studies showed that
466 afucosylated antibodies have a much higher affinity (100-fold) for FcγRIIIa (CD16a) and may thus
467 have enhanced ADCC [84]. Moreover, ADCC via FcγRIIIa may require NK cells, but not monocytes
468 or polymorphonuclear cells, and activity levels of the antigen/antibody/effector cell complexes have
469 been correlated only with the NK cell numbers present in the PBMC [20]. Our associations between
470 the levels of IgG core fucose and of a subpopulation of NK cells reinforce the notion that there is a
471 complementarity between IgG core fucose levels and NK cells, that could influence effector cell
472 potency, potentially against a range of antigens including self-antigens.
473 It has been previously estimated that AITD are highly heritable (55-75%) and that most of
474 IgG N-glycan traits and the immune cell traits associated with AITD are moderately heritable (**Table**
475 **S8)** [4,27]. By estimating the proportion of genetic and environmental variance of 1,129 proteins in
476 our study using the Structural Equation Modeling and twin structures present in the TwinsUK cohort
477 (**Table S9**), we found a small proportion of proteins having additive genetic variances in their
478 heritability, in concordance with previous findings on a smaller dataset [85]. As the best model of
479 heritability in AITD is only with dominant genetic variance, the shared genetic variance between
480 AITD and proteins as well as with IgG N-glycan traits and immune cell traits could not be estimated
481 with accuracy. However, in our study, we identified several genetic variants previously associated
482 with thyroid phenotypes to be also associated with the secretion of proteins and gene expression of
483 ligands of two NK cell immunoreceptors. Specifically, genetic variants, rs1521 and rs3094228,
484 associated with Graves' disease and TPOAb-positivity, alter the expression of thyroid cell-expressed
485 ligands, *MIC-A, MIC-B,* and *HLA-C*, known to recognize CD314 and CD158b immunoreceptors
486 expressed on NK cells. Moreover, rs3094228 falls in the same European haplotype as three genetic
487 variants associated with higher abundance of the activated $CD158b^{+}CD314^{+}CD335^{-}$ NK cell subset.
488 Thus, individuals having the AITD-risk allele of rs1521 variant have reduced expression of *HLA-C*
489 gene and, at a lesser extent, expression of *MIC-A* in thyrocytes, whereas the carriers of AITD-risk
490 allele of rs3094228 genetic variant associated with TPOAb-positivity showed increased expression of
491 *MIC-B* gene in thyrocytes and potentially higher abundance of the highly active
492 $CD158b^{+}CD314^{+}CD335^{-}$ NK cells. Consequently, if the thyrocytes in carriers of AITD-risk alleles for
493 CD158b and CD314 ligands crosstalk with the subpopulation of NK cells with CD158b and CD314
494 immunoreceptors with the help of the antibodies, they could trigger the production of cytokines and
495 cytotoxicity against thyrocytes by these NK cells.
496 Our findings thus highlight different immune features (glycan structures on antibodies, a
497 subpopulation of immunoactive NK cells, the secretion of Caspase-2 and IL-1α) as potential signals
498 of AITD status detectable in the bloodstream in addition to TSH and TPOAb levels. Moreover, if one
499 speculates that active antibodies with low core-fucose might be thyroid autoantibodies (e.g., TPOAb)
500 [86] and target cells are thyroid cells, it is conceivable (**Fig. 5**) that that immune cell-antibody-target
501 cell interactions may lead to cytotoxicity functions targeting thyroid tissues [76,86,87]. Together, these
502 may form part of a dysregulated autoimmune response in AITD**.** Further replication studies and
503 validation studies of real-time functional evaluations associated with these immune features and
504 genetic analyses are needed to confirm this model. These features could also be tested in the context
505 of thyroid cancer immunotherapy [77] in future studies.

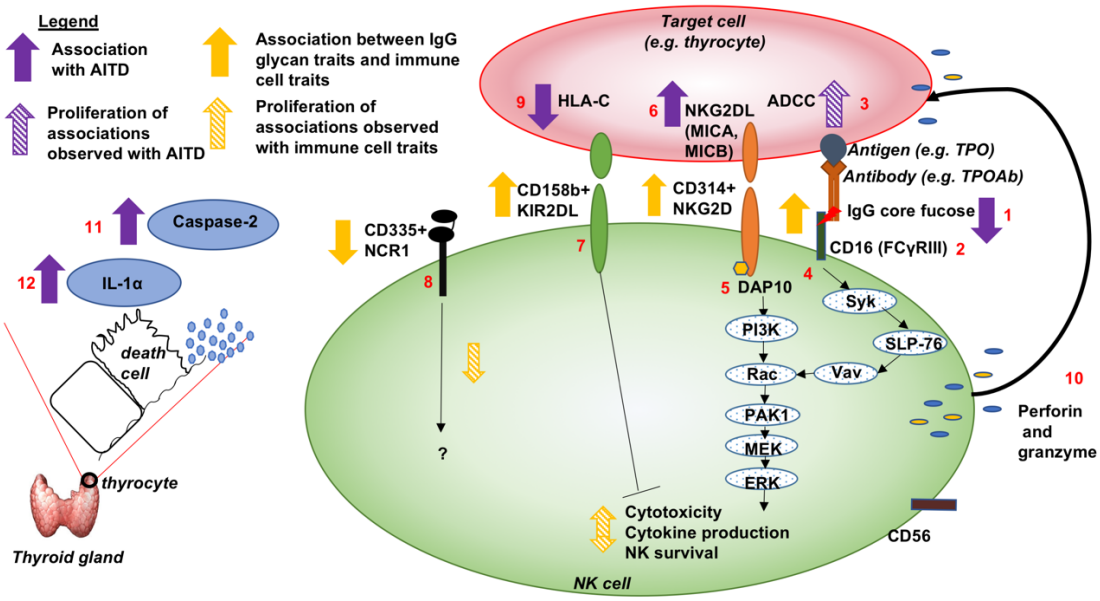

Figure 5. Model of different potential contributing players and their pathways activated in proposed antibody-dependent NK cell-mediated cytotoxicity in the thyroid gland of AITD patients. 1) The depletion of IgG core fucose was associated with TPOAb level and AITD status [4]. 2) The IgG N-glycan traits associated with AITD were also associated with a subpopulation of NK cells in our current study; for example, the depletion of IgG core fucose is associated positively with NK cells with the patterns of co-receptors CD335- or CD335-CD158b+CD314+. 3) Previous studies showed that afucosylated antibodies had increased affinity for binding to CD16 (FcγRIIIa), cell receptors of NK cells, and to enhance ADCC [18–21] via 4) protein tyrosine kinase-dependent pathways, through crosstalk with 5) NKG2D receptor (CD314) [88,89]. 6) Two SNPs, rs3094228 and rs1521, were associated with GD and TPOAb-positivity [60–62] and fall in gene regulatory regions of the *MIC-A* and *MIC-B* genes and increase their expression in thyroid cells [32]. These two genes encode heavily glycosylated proteins that are ligands for the NKG2D type II receptor (CD314). 7) The KIR2DL (CD158b) receptor is known to regulate the cytotoxicity of NK cells by unknown pathways, whereas 8) the NCR1 (CD335) receptor can contribute to the increased potency of activated NK cells to mediate cell lysis by unknown pathway [54,55]. 9) The SNP, rs1521 associated with GD[60], is also shown to reduce the expression of HLA-C gene, producing the ligand of CD158b, in thyroid cells [32,33,58,59]. 10) All together (the binding of NK cells with target cells through antibodies and their ligands), these lead to the activation of NK cells, which release cytotoxic granules containing perforin and granzymes. This release mediates ADCC of target cells (3), which are thyrocytes in AITD. Also, 11) a positive association between the circulation abundance of Caspase-2 protein and AITD were found in this study that could be associated with the destruction of thyrocytes. 12) A positive correlation of circulating abundance of IL-1α with AITD was also found in the bloodstream that could be a marker of lymphocyte infiltration in the thyroid gland of individuals with AITD, and thus of inflammation [80,81].

Supplementary Materials: The following are available online at www.mdpi.com/xxx/s1,

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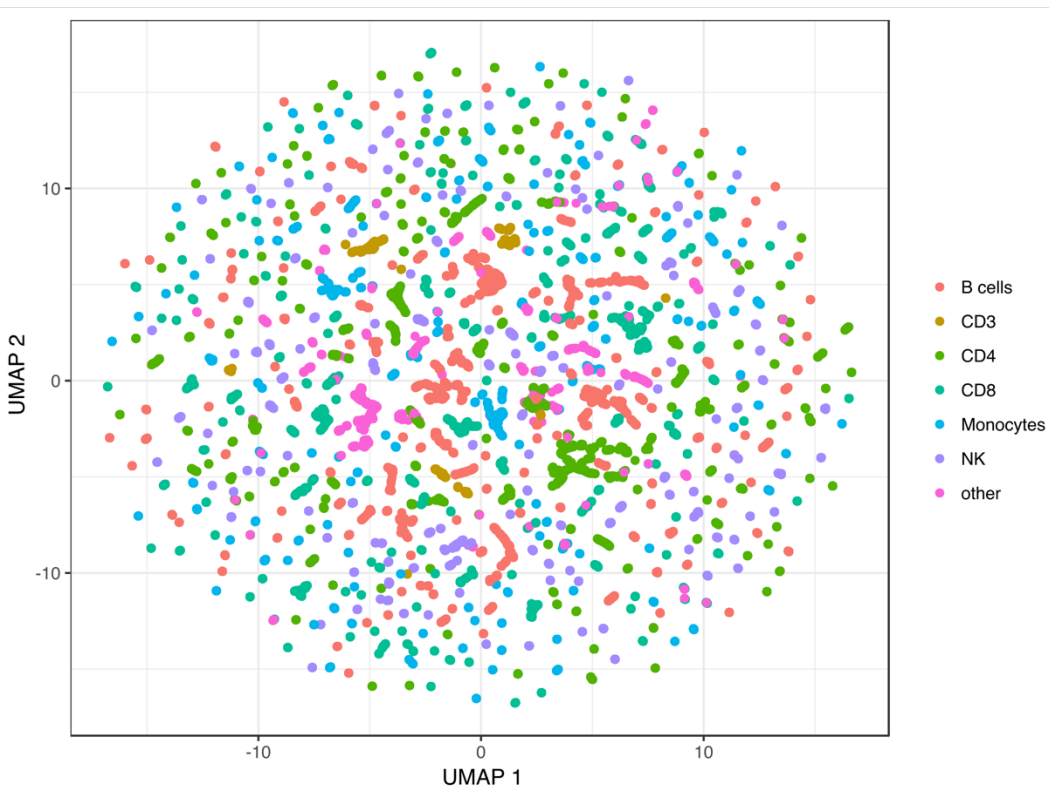

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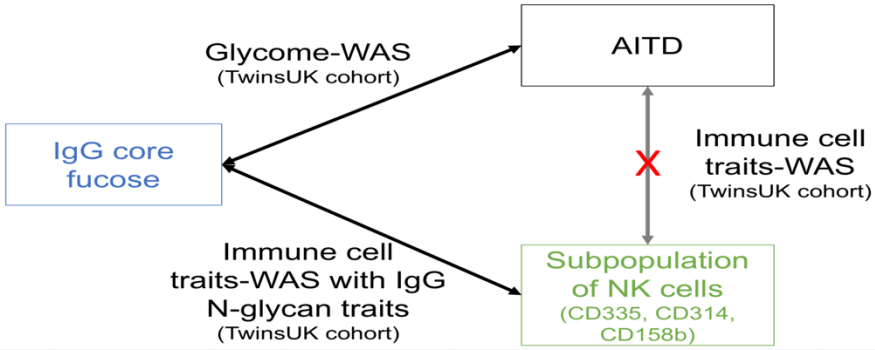

Analysis	Data source (sample size)	Tissue	Exposure	outcome	Sign of Beta value	P-value
Glycome-WAS*	TwinsUK cohort (n=2,297), Polish cohort (n=219) and Croatian cohort (n=163)	plasma	AITD status/ TPOAb level	11 core fucose IgG N-glycan traits (IGP7, IGP8, IGP15, IGP33, IGP48, IGP56, IGP58, IGP59, IGP60, IGP62 and IGP63)	-	$<2.5x10^{-3}$
				6 core afucose IgG N-glycan traits (IGP2, IGP21, IGP36, IGP42, IGP45, IGP46)	+	
Immune cell traits-WAS with IgG N-glycan traits	TwinsUK cohort (n=383)	plasma	3 core fucose IgG N-glycan traits (IGP58,IGP59, IGP60)	NK cells 16+56+/CD335- (CD314+, CD158b+)	-	$<2.4x10^{-6}$
				NK cells 16+56+/CD335+ (CD158b-)	+	
			3 core afucosed IgG N-glycan traits (IGP2,IGP42, IGP46)	NK cells 16+56+/CD335- (CD314+, CD158b+)	+	
				NK cells 16+56+/CD335+ (CD158b-)	-	
Immune cell traits-WAS	TwinsUK cohort (n=374)	plasma	AITD status/ TPOAb level	51 immune cell traits (NK cells – CD335, CD314, CD158b)	NS	>0.05

Figure S1: Immune cell traits and AITD status. (a) Immune cell traits were arranged in two dimensions based on the similarity of their quantification profiles by the dimensionality reduction technique UMAP [72] using R package umapr [73]. Some clusters that emerge spontaneously can be associated with specific immune cell types (colors). (b) Overview of associations observed between IgG core-fucose, a subpopulation of NK cells and AITD status in the TwinsUK cohort. *Glycome-wide association studies of AITD and TPOAb levels were previously performed [4].

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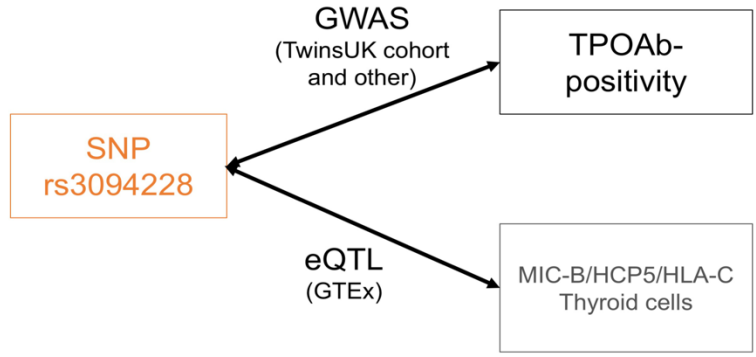

Analysis	Data source (sample size)	Tissue	Exposure	outcome	Beta value	P-value
GWAS*	TwinsUK cohort (n=2,297)	plasma	rs3094228	TPOAb-positivity	1.23	$<5\times10^{-8}$
eQTL**	GTEx (n=948)	thyroid	rs3094228	MIC-B Gene expression	0.26	3.7×10^{-9}
				HCP5 Gene expression	-0.24	3.0×10^{-8}
				HLA-C Gene expression	0.25	9.3×10^{-7}

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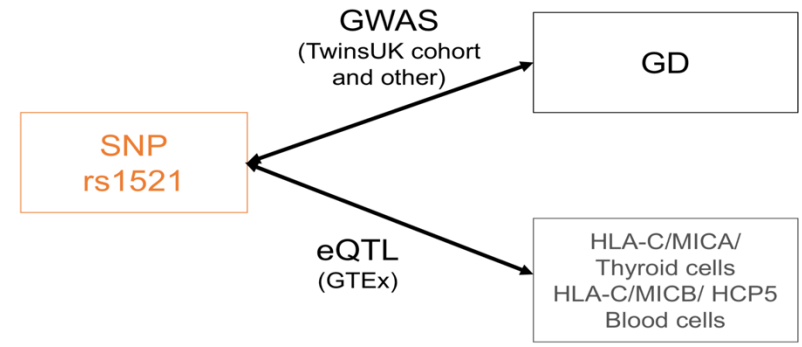
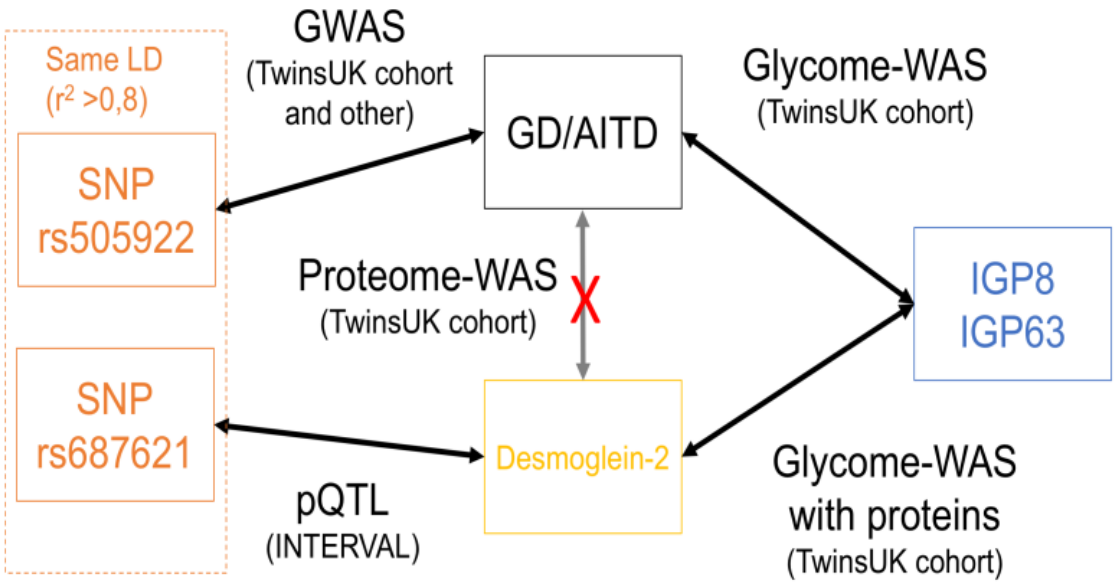


Analysis	Data source (sample size)	Tissue	Exposure	outcome	Beta value	P-value
GWAS*	TwinsUK cohort (n=2,297)	plasma	rs1521	GD	1.23	$<5\times10^{-8}$
eQTL**	GTEx (n=948, thyroid; n=948, whole blood)	Thyroid	rs1521	HLA-C Gene expression	-0.24	8.2×10^{-8}
				MIC-A Gene expression	-0.18	2.5×10^{-5}
	Westra (n=8086, whole blood)	Whole blood	rs1521	HLA-C Gene expression	-0.12	5.7×10^{-5}
				MIC-B Gene expression	NA	5.2×10^{-4}
				HCP5 Gene expression	NA	4.6×10^{-6}

Figure S2. Overview of associations between AITD-SNP and eQTL in thyroid and blood cells. *Genome-wide association studies of AITD and TPOAb-positivity were previously performed, and the findings are available via GWAS catalog [30] whereas **eQTLs come from GTEx project [34] and Westra and al. [35]. (a) Associations between AITD-SNP and eQTL in thyroid and blood cells for the genetic variant rs3094228. (b) Associations between AITD-SNP and eQTL in thyroid and blood cells for the genetic variant rs1521.



Analysis	Data source (sample size)	Tissue	Exposure	outcome	Beta value/ OR	P-value
GWAS*	TwinsUK cohort (n=2,297)	plasma	rs505922	GD	1.13	$<2.5\times10^{-3}$
Protein-quantitative trait loci**	INTERVAL (n=3,301)	plasma	rs687621	Desmoglein-2	0.20	1.9×10^{-11}
Protein-WAS	TwinsUK cohort (n= up to 348)	plasma	AITD status/ TPOAb level	Desmoglein-2	NS	$>1.9\times10^{-4}$
Glycome-WAS***	TwinsUK cohort (n=2,297), Polish cohort (n=219) and Croatian cohort (n=163)	plasma	AITD status/ TPOAb level	IGP8	-6.93	2.1×10^{-3}
				IGP63	-7.23	1.2×10^{-3}
Protein-WAS	TwinsUK cohort (n= 164)	plasma	IGP8	Desmoglein-2	0.032	2.2×10^{-6}
			IGP63	Desmoglein-2	0.032	8.0×10^{-6}

Figure S3. Overview of multi-omic findings associated with Desmoglein-2 in individuals with AITD status and general population. We highlighted a locus with high LD having SNPs and two IgG glycan traits that are both associated with GD and the abundance of secreted plasma Desmoglein-2 in plasma. However, no direct association of AITD status with the abundance of secreted plasma Desmoglein-2. We previously performed glycome-wide association studies of AITD and TPOAb levels [4]. Genome-wide association studies of AITD and TPOAb-positivity were previously performed, and the findings are available via GWAS catalog [30] whereas pQTLs come from INTERVAL project[31]. IGP8 = the percentage of FA2[3]G1 glycan in total IgG glycans. IGP63 = The percentage of fucosylation (without bisecting GlcNAc) of agalactosylated structures.

Table S1: Description of TwinsUK cohort used for different analysis performed here

Table S2: Significant glycome associations with immune cell traits in the TwinsUK cohort

Table S3: Associations of 51 immune cell traits with AITD and TPOAb level in the TwinsUK cohort

Table S4: Hits from selected eQTL studies for two SNPs, rs1521 and rs3094228 in the thyroid cells and whole blood

Table S5: Genes reported for genetic variants associated with thyroid phenotypes and immune cell traits

Table S6: Glycome-wide associations studies of 17 AITD-IgG N-glycan traits with 1,113 circulating proteins. Only significant ones were put here.

Table S7: Genetic variants associated with thyroid phenotypes and AITD-IgG N-glycan traits overlapping pQTL identified in INTERVAL project (LD r^2>0.8)

Table S8: Heritability of AITD, 17 IgG N-glycan traits and 51 immune cell traits in the TwinsUK cohort

Table S9: Heritability of 1,113 proteins in the TwinsUK cohort

Abbreviations. ADCC (Antibody-Dependent Cell-mediated Cytotoxicity), AITD (AutoImmune Thyroid Diseases), CDC (Complement-Dependent Cytotoxicity), CD158b (KIR2DL2/L3 - Killer Cell Immunoglobulin Like Receptor, Two Ig Domains And Long Cytoplasmic Tail 2 or 3 - or NKAT6 - Natural Killer-Associated Transcript 6), CD314 (NKG2D or KLRK1 - Killer Cell Lectin Like Receptor K1), eQTL (gene Expression Quantitative Trait Loci), FcγR (Fc gamma Receptor), GD (Graves' Diseases), GlcNAc (N-acetylglucosamine), GWAS (Genome-wide Association Study), HT (Hashimoto's thyroiditis), IgG (Immunoglobulin G), MIC-A (MHC Class I Polypeptide-Related Sequence A), MIC-B (MHC Class I Polypeptide-Related Sequence B), NK (Natural Killer cell), PBMC (Peripheral Blood Mononuclear Cells), pQTL (Protein expression Quantitative Trait Loci), Tg (Thyroglobulin), TSH (Thyroid-Stimulating Hormone), TSH-R (Thyroid-Stimulating Hormone Receptor), TPO (Thyroid PerOxidase), TPOAb (TPO Antibody).

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Appendix A

A.1. Detection of TSH and TPOAb in human sera

Sera to assess TPOAb and TSH levels were collected by a trained nurse or phlebotomist using venepuncture and a SafetyLokTM Blood Collection Kit (21G3/4 Needles) and plain 10 ml serum-separating tube vacutainer (no additives) between February 1994 and May 2007. After collection from the study subject, whole blood was held at 22°C for 50 min at room temperature for a clot to form and serum separated within 60 minutes of collection. Processing of blood was performed using a refrigerated (4°C) clinical centrifuge at 3000xg for 10 minutes with the serum supernatant subsequently collected, transferred to a 2ml screw capped Nunc Cryotubes and immediately frozen at -80°C and kept frozen in 2ml screw capped Nunc Cryotube at -80°C until use. Quantitative determination of TSH and TPOAb (only IgG class) levels was performed on the sera either by a chemiluminescent microparticle immunoassay (CMIA) [ARCHITECT® Anti-TPO or TSH (ABBOTT Diagnostics Division, Wiesbaden, Germany, 2005)] (TPOAb titer>6 mIU/L considered positive; reference range for TSH level 0.4-4.0 mIU/L) or by an electrochemiluminescence immunoassay "ECLIA" [Elecsys and Cobas e analyzers, (Roche Diagnostics, Indianapolis, lN, USA, 2010)] (TPOAb titer>34 IU/mL considered positive; reference range for TSH 0.4-4.0 mIU/L).

A.2. Detection of IgG glycosylation profiling

For IgG glycosylation analysis, using UPLC analysis of 2AB-labelled glycans, chromatograms were separated in the same manner into 24 peaks, and the amount of glycans in each peak was expressed as a percentage of the total integrated area. One glycan was excluded before any transformation and standardization of data because of its co-elution with a contaminant that significantly affected its values in some samples whereas two glycan peaks (GP) GP20 and GP21 (Zagreb code) were combined into a single trait called GP2021 (Zagreb code) because of difficulty in distinguishing between these peaks in some samples. A global normalization and natural logarithm transformation were applied to 22 directly measured glycan structures. As many of these structures share the same structural features (galactose, sialic acid, core-fucose, bisecting N-acetylglucosamine (GlcNAc)), 55 additional derived traits were calculated that average these features across multiple glycans from the 22 normalized and non-transformed directly measured glycans. Technical confounders (batch and run-day effects) were addressed using R package ComBat. The 22 directly measured glycans and 55 derived glycan traits were centered and scaled to have a mean of 0 and standard deviation (SD) of 1. Samples being more than 6 SD from the mean were considered as outliers and excluded from the analysis.

A.3. Detection of protein profiling in plasma

Plasma protein profiling was conducted using SOMAscan v2 (SomaLogic Inc, Boulder, CO) as previously described [29,30]. Briefly, hemolyzed samples were first excluded. Proteins were then measured using a SOMAmer-based capture array called "SOMAscan." Quality control was performed at the sample and SOMAmer level and involves the use of control SOMAmers on the microarray and calibration samples. At the sample level, hybridization controls on the microarray are used to monitor sample-by-sample variability in hybridization, while the median signal over all SOMAmers is used to monitor overall technical variability. The resulting hybridization scale factor and median scale factor are used to normalize data across samples. The acceptance criteria for these values are 0.4–2.5, based on historical trends in these values. Somamer-by-somamer calibration occurs through the repeated measurement of calibration samples; these samples are of the same

matrix as the study samples and are used to monitor repeatability and batch to batch variability. Historical values for these calibrator samples for each SOMAmer are used to generate a calibration scale factor. The acceptance criteria for calibrator scale factors is that 95% of SOMAmers must have a calibration scale factor within ±0.4 of the median. For the current analysis, only 1,113 proteins were then studied.

A.4. Selection of SNPs associated with immune cell traits

To define the list of SNPs associated with immune cell traits regardless to any specific phenotypes in the TwinsUK cohort, we extracted SNPs for each immune cell traits that have a P-value under GWAS P-value threshold (P-value < $5x10^{-8}$) from previous published GWASs on these immune cell traits [27,28]. To define the list of SNPs associated with protein abundance found in this study, we extracted the significant SNPs reported in INTERVAL project [31]. To define the list of SNPs associated with gene expression (eQTL), we extracted the eQTLs reported significant by GTEx and previous papers present in HaploReg V4.1 [47]. To define the list of SNPs associated with AITD and thyroid functions, we selected to SNPs listed in the NHGRI GWAS catalog [52] with words "thyroid" or "Graves" or "Hashimoto."

A.5. Determination of effective number of independent tests for different -omic data

Due to high and partial correlations within glycans, proteins and immune cell traits, we decided to use the equation 5 proposed by Li & Ji ((2005) [45] to define an effective number (M_{eff}) of independent tests. We then used this number to define the effective Bonferroni P-value threshold such as $0.05/M_{eff}$ instead of 0.05/M, with M the actual number of tests. 20 independent tests were estimated for 76 glycans. Consequently, to account for multiple testing in the discovery cohort, we present results surpassing a conservative Bonferroni correction assuming 20 independent tests, thus giving a significant threshold of (P-value <$2.5x10^{-3}$=0.05/20). 1,357 independent tests were estimated for 23,485 immune cell traits, thus giving a significant threshold of $3.68x10^{-5}$ (0.05/1,357). 227 independent tests were estimated among 1,113 proteins (P<0.05/227=1.9x10-4).

A.6. Association studies between -omics features and thyroid phenotypes

To examine whether one of the 17 AITD-IgG N-glycan traits was significantly associated with one of the 23,485 immune cell traits, we compared the fitted model in equation (2) with a model that did not include the residual of glycan in equation (1):

$$\text{Model null:} \quad Y_i \sim a + h\,(\text{fixe intercepts}) + g\,(\text{random intercepts}) + \varepsilon_{ij} \qquad (1)$$

$$\text{Model 1:} \quad Y_i \sim a + \mathbf{bG}_{ij} + h\,(\text{fixe intercepts}) + g\,(\text{random intercepts}) + \varepsilon_{ij} \qquad (2)$$

Where Y_i represents the quantification of immune cell traits for individual *i* and Gij is glycan structure of type *j* among 75 *N*-glycans for the same individual i. If biological covariates (age, sex) have not been adjusted before association analysis, they have been added in the model. A random intercept was added only in the discovery cohort in order to model the family-relatedness.

To examine whether an immune cell trait was significantly associated with TPOAb level and AITD status, we compared the fitted model in equation (2) with a model that did not include the immune cell traits in equation (1) where Gij become the immune cell trait of type j among 23,485 in discovery cohort for the same individual i. For the discovery and replication cohorts in TwinsUK, we added a random intercept in order to model the family-relatedness.

To examine whether one of the 1,113 protein was significantly associated with TPOAb level and AITD status, we compared the fitted model in equation (2) with a model that did not include the protein in equation (1): where Gij become the protein of type j among 1,129 in discovery cohort for the same individual i. We added a random intercept in order to model the family-relatedness. To examine whether one of 1,113 proteins was significantly associated with one of 17 significant glycans, we compared the fitted model in equation (2) with a model that did not include the protein in equation (1): where Gij become the protein of type j among 1,129 in discovery cohort for the same individual i. We added a random intercept in order to model the family-relatedness.

11.7. Heritability analysis for proteins

Using twin data and ADCE models (additive genetics (A), dominante genetics (D), shared environment (C) and non-shared environment (E)), heritability of glycosylation structures, immune cell traits and AITD were estimated using the R package called mets that allows us to run the analysis with monozygotic and dizygotic twins as well as unrelated individuals. The significance of variance components A, D, and C was assessed by dropping each component sequentially from the full model (ADCE) and comparing the sub-model fit to the full model. Sub-models were compared to full models by hierarchical χ^2 tests. The difference between log-likelihood values between sub-model and full model is asymptotically distributed as χ^2 with degrees of freedom (df) equal to the difference in df of sub-model and the full model. A statistical indicator of goodness-of-fit is the Akaike information criterion (AIC), computed as χ^2 - 2df; sub-models are accepted as the best-fitting model if there is no significant loss of fit when a latent variable (A, C, D, or E) is fixed to equal zero. When two sub-models have the same AIC compared to the full model, we decide to keep the model the most likely (with additive genetic variance) or with the lowest P-value for different components.

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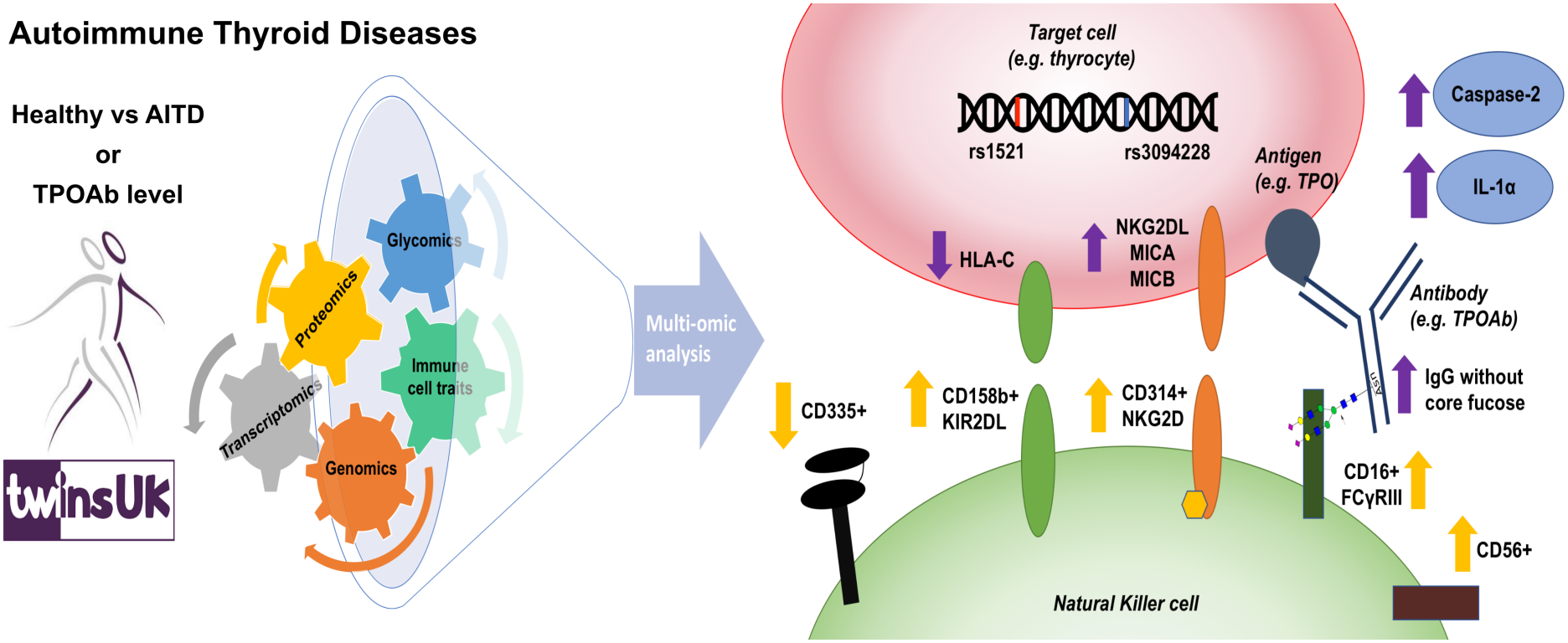
Autoimmune Thyroid Diseases
Healthy vs AITD
or
TPOAb level
twinsUK
Glycomics
Proteomics
Immune cell traits
Transcriptomics
Genomics
Multi-omic analysis
Target cell
(e.g. thyrocyte)
rs1521
rs3094228
Antigen
(e.g. TPO)
Caspase-2
IL-1α
HLA-C
NKG2DL
MICA
MICB
Antibody
(e.g. TPOAb)
IgG without
core fucose
CD335+
CD158b+
KIR2DL
CD314+
NKG2D
CD16+
FCγRIII
CD56+
Natural Killer cell

Table S1: Description of TwinsUK cohort used for different analysis performed here

* Roederer, M et al., Cell, 2015, doi: 10.1016/j.cell.2015.02.046 and Mangino et al, Nature Communications, 2017, https://doi.org/10.1038/ncomms13850

Analysis	GWAS on immune cell traits*	Immune-wide association studies with thyroid phenotypes					immune cell traits-wide association studies with IgG N-glycan traits	Proteome-wide association studies with thyroid phenotypes					Glycome-wide association studies with proteins
Phenotype		TPOAb	AITD					TPOAb	AITD				
Group		continuous	control		case			continuous	control		case		
TPOAb immunoassay	NA	Roche	Abbott	Roche	Abbott	Roche	NA	Roche	Abbott	Roche	Abbott	Roche	NA
threshold of TPOAb-positivity (UI/mL)	NA	34	6	34	6	34	NA	34	6	34	6	34	NA
Number of individuals	497	374	77	127	19	22	383	155	25	105	9	18	164
Age (mean/sd)	60 (8.2)	55.8 (8.4)	52.59 (7.20)	55.41 (8.4)	51.58 (7.49)	53.40 (8.02)	60 (8.2)	61.19 (6.96)	56.59 (8.10)	61.64 (7.8)	55.20 (4.65)	60.66 (6.73)	64.20 (7.27)
Sex (F/M)	497/0	374/0	77/0	127/0	19/0	22/0	383/0	155/0	25/0	105/0	9/0	18/0	164/0
TPOAb (mean/sd)	NA	50.5 (108.4)	1.42 (8.49)	10.50 (5.37)	463.86 (568.45)	312.68 (146.01)	NA	66.65 (36.19)	0.14 (0.37)	9.33 (5.05)	585.66 (1156.48)	324.81 (147.69)	NA

Table S2: Significant glycome associations with immune cell traits in the TwinsUK cohort
SE=standart error

Glycan ID	Description	immuneTrait ID	Trait ID	Canonical name	Lineage	Subset name	Pvalue	Beta	SE	Zscore
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	9.22E-08	0.285	0.052	5.445
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	5.10E-08	0.277	0.050	5.555
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	9.29E-08	0.237	0.044	5.443
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	7.88E-08	-0.228	0.042	-5.477
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	8.11E-08	-0.234	0.043	-5.468
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	2.14E-08	-0.242	0.042	-5.718
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	8.47E-08	0.286	0.052	5.461
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	4.69E-08	0.278	0.050	5.571
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	8.94E-08	0.237	0.044	5.451
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	7.49E-08	-0.228	0.042	-5.487
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	7.62E-08	-0.234	0.043	-5.480
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	2.03E-08	-0.243	0.042	-5.728
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	9.58E-08	0.285	0.052	5.437
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	5.24E-08	0.277	0.050	5.550
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	9.70E-08	0.237	0.044	5.435
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	8.37E-08	-0.227	0.042	-5.466
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	8.77E-08	-0.233	0.043	-5.454
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	2.28E-08	-0.242	0.042	-5.706
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	8.51E-08	0.286	0.052	5.460
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	4.64E-08	0.278	0.050	5.573
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	8.68E-08	0.238	0.044	5.456
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	7.57E-08	-0.228	0.042	-5.485
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	7.85E-08	-0.234	0.043	-5.475
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	2.06E-08	-0.243	0.042	-5.726
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_62860	P4:18	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-R	8.79E-07	-0.250	0.050	-4.999
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_62860	P4:18	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-R	8.06E-07	-0.240	0.048	-5.025
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_62860	P4:18	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-R	5.26E-07	0.208	0.040	5.154
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	1.77E-08	-0.284	0.049	-5.752
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	9.79E-09	-0.275	0.047	-5.863
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	4.86E-07	-0.211	0.041	-5.131
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	3.67E-07	0.202	0.039	5.183
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	7.23E-07	0.204	0.040	5.044
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	6.14E-08	0.221	0.040	5.540
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63596	P4:2461	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-R7-	4.61E-07	-0.256	0.050	-5.134
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63596	P4:2461	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-R7-	3.39E-07	-0.248	0.048	-5.206
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63596	P4:2461	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-R7-	4.44E-07	0.210	0.040	5.189
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63597	P4:2462	NK Activating 2	16+56	16+56/314+335+337-158a-158b-R7-	5.91E-08	-0.276	0.050	-5.527
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63597	P4:2462	NK Activating 2	16+56	16+56/314+335+337-158a-158b-R7-	4.89E-08	-0.264	0.047	-5.565
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63597	P4:2462	NK Activating 2	16+56	16+56/314+335+337-158a-158b-R7-	1.61E-06	-0.203	0.042	-4.891
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63597	P4:2462	NK Activating 2	16+56	16+56/314+335+337-158a-158b-R7-	2.99E-07	0.212	0.040	5.239
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	4.19E-08	-0.278	0.050	-5.594
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	2.47E-08	-0.269	0.047	-5.697
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	1.23E-06	-0.205	0.041	-4.945
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	1.19E-06	0.195	0.039	4.948
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	2.07E-07	0.214	0.040	5.312
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63623	P4:2486	NK Activating 2	16+56	16+56/CD2+335+158a-158b-R7-	8.58E-07	-0.250	0.050	-5.010
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63623	P4:2486	NK Activating 2	16+56	16+56/CD2+335+158a-158b-R7-	6.33E-07	-0.242	0.048	-5.082
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63623	P4:2486	NK Activating 2	16+56	16+56/CD2+335+158a-158b-R7-	7.60E-07	0.206	0.040	5.082
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63625	P4:2488	NK Activating 2	16+56	16+56/314+335+158a-158b-R7-	9.03E-08	-0.272	0.050	-5.447
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63625	P4:2488	NK Activating 2	16+56	16+56/314+335+158a-158b-R7-	7.32E-08	-0.261	0.048	-5.490
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63625	P4:2488	NK Activating 2	16+56	16+56/314+335+158a-158b-R7-	4.19E-07	0.210	0.041	5.173
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63626	P4:2489	NK Activating 2	16+56	16+56/CD2+314+335+158a-158b-R7-	1.54E-06	-0.245	0.050	-4.885
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63626	P4:2489	NK Activating 2	16+56	16+56/CD2+314+335+158a-158b-R7-	1.34E-06	-0.236	0.048	-4.921
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63626	P4:2489	NK Activating 2	16+56	16+56/CD2+314+335+158a-158b-R7-	8.03E-07	0.206	0.041	5.070
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63674	P4:2531	NK Activating 2	16+56	16+56/335+337-158b-R7-	4.62E-09	-0.282	0.047	-5.994
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63674	P4:2531	NK Activating 2	16+56	16+56/335+337-158b-R7-	2.85E-09	-0.272	0.045	-6.079
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63674	P4:2531	NK Activating 2	16+56	16+56/335+337-158b-R7-	2.26E-07	-0.207	0.039	-5.276
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63674	P4:2531	NK Activating 2	16+56	16+56/335+337-158b-R7-	1.79E-07	0.198	0.037	5.319
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_63674	P4:2531	NK Activating 2	16+56	16+56/335+337-158b-R7-	4.57E-07	0.198	0.039	5.131
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63674	P4:2531	NK Activating 2	16+56	16+56/335+337-158b-R7-	3.49E-08	0.215	0.038	5.638

IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63675	P4:2532	NK Activating 2	16+56	16+56/CD2+335+337-158b-R7-	2.26E-07	-0.251	0.048	-5.270
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63675	P4:2532	NK Activating 2	16+56	16+56/CD2+335+337-158b-R7-	1.72E-07	-0.241	0.045	-5.333
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63675	P4:2532	NK Activating 2	16+56	16+56/CD2+335+337-158b-R7-	1.62E-06	0.184	0.038	4.902
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63675	P4:2532	NK Activating 2	16+56	16+56/CD2+335+337-158b-R7-	4.20E-07	0.200	0.038	5.190
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63677	P4:2534	NK Activating 2	16+56	16+56/314+335+337-158b-R7-	1.42E-08	-0.275	0.048	-5.793
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63677	P4:2534	NK Activating 2	16+56	16+56/314+335+337-158b-R7-	1.37E-08	-0.262	0.045	-5.798
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63677	P4:2534	NK Activating 2	16+56	16+56/314+335+337-158b-R7-	7.02E-07	-0.200	0.040	-5.052
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63677	P4:2534	NK Activating 2	16+56	16+56/314+335+337-158b-R7-	8.60E-07	0.189	0.038	5.008
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63677	P4:2534	NK Activating 2	16+56	16+56/314+335+337-158b-R7-	1.39E-07	0.207	0.039	5.377
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63678	P4:2535	NK Activating 2	16+56	16+56/CD2+314+335+337-158b-R7-	3.64E-07	-0.248	0.048	-5.174
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63678	P4:2535	NK Activating 2	16+56	16+56/CD2+314+335+337-158b-R7-	3.79E-07	-0.236	0.046	-5.172
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63678	P4:2535	NK Activating 2	16+56	16+56/CD2+314+335+337-158b-R7-	5.68E-07	0.199	0.039	5.129
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63703	P4:2558	NK Activating 2	16+56	16+56/335+158b-R7-	6.83E-09	-0.280	0.047	-5.924
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63703	P4:2558	NK Activating 2	16+56	16+56/335+158b-R7-	4.04E-09	-0.270	0.045	-6.017
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63703	P4:2558	NK Activating 2	16+56	16+56/335+158b-R7-	2.97E-07	-0.205	0.039	-5.224
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63703	P4:2558	NK Activating 2	16+56	16+56/335+158b-R7-	2.41E-07	0.197	0.037	5.262
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_63703	P4:2558	NK Activating 2	16+56	16+56/335+158b-R7-	6.17E-07	0.196	0.039	5.071
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63703	P4:2558	NK Activating 2	16+56	16+56/335+158b-R7-	4.67E-08	0.214	0.038	5.585
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63704	P4:2559	NK Activating 2	16+56	16+56/CD2+335+158b-R7-	3.13E-07	-0.248	0.048	-5.206
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63704	P4:2559	NK Activating 2	16+56	16+56/CD2+335+158b-R7-	2.36E-07	-0.239	0.045	-5.271
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63704	P4:2559	NK Activating 2	16+56	16+56/CD2+335+158b-R7-	5.59E-07	0.198	0.039	5.133
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63707	P4:2561	NK Activating 2	16+56	16+56/314+335+158b-R7-	1.98E-08	-0.272	0.048	-5.731
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63707	P4:2561	NK Activating 2	16+56	16+56/314+335+158b-R7-	1.94E-08	-0.259	0.045	-5.734
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_63707	P4:2561	NK Activating 2	16+56	16+56/314+335+158b-R7-	1.06E-06	-0.197	0.040	-4.969
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_63707	P4:2561	NK Activating 2	16+56	16+56/314+335+158b-R7-	1.29E-06	0.185	0.038	4.925
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63707	P4:2561	NK Activating 2	16+56	16+56/314+335+158b-R7-	2.06E-07	0.204	0.039	5.303
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63708	P4:2562	NK Activating 2	16+56	16+56/CD2+314+335+158b-R7-	4.66E-07	-0.246	0.048	-5.125
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63708	P4:2562	NK Activating 2	16+56	16+56/CD2+314+335+158b-R7-	4.49E-07	-0.235	0.046	-5.138
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_63708	P4:2562	NK Activating 2	16+56	16+56/CD2+314+335+158b-R7-	6.39E-07	0.198	0.039	5.105
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63835	P4:2677	NK Activating 2	16+56	16+56/335+337-158a-R7-	1.61E-06	-0.222	0.045	-4.881
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63925	P4:2758	NK Activating 2	16+56	16+56/335+337-R7-	1.32E-06	-0.210	0.043	-4.916
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64341	P4:3131	NK Activating 2	16+56	16+56/335+337-158a-158b-	1.57E-08	-0.286	0.050	-5.775
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64341	P4:3131	NK Activating 2	16+56	16+56/335+337-158a-158b-	8.68E-09	-0.277	0.047	-5.885
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64341	P4:3131	NK Activating 2	16+56	16+56/335+337-158a-158b-	5.85E-07	-0.210	0.041	-5.094
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64341	P4:3131	NK Activating 2	16+56	16+56/335+337-158a-158b-	4.26E-07	0.202	0.039	5.154
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64341	P4:3131	NK Activating 2	16+56	16+56/335+337-158a-158b-	7.39E-07	0.205	0.041	5.040
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64341	P4:3131	NK Activating 2	16+56	16+56/335+337-158a-158b-	7.26E-08	0.221	0.040	5.509
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64342	P4:3132	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-	4.75E-07	-0.256	0.050	-5.128
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64342	P4:3132	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-	3.55E-07	-0.247	0.048	-5.196
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64342	P4:3132	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-	4.46E-07	0.210	0.040	5.186
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64344	P4:3134	NK Activating 2	16+56	16+56/314+335+337-158a-158b-	4.41E-08	-0.278	0.050	-5.582
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64344	P4:3134	NK Activating 2	16+56	16+56/314+335+337-158a-158b-	3.59E-08	-0.267	0.047	-5.623
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64344	P4:3134	NK Activating 2	16+56	16+56/314+335+337-158a-158b-	1.38E-06	-0.205	0.042	-4.921
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64344	P4:3134	NK Activating 2	16+56	16+56/314+335+337-158a-158b-	1.59E-06	0.194	0.040	4.887
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64344	P4:3134	NK Activating 2	16+56	16+56/314+335+337-158a-158b-	2.30E-07	0.214	0.040	5.290
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64345	P4:3135	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-	7.22E-07	-0.252	0.050	-5.040
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64345	P4:3135	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-	6.52E-07	-0.242	0.048	-5.068
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64345	P4:3135	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-	3.94E-07	0.211	0.040	5.211
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64370	P4:3158	NK Activating 2	16+56	16+56/335+158a-158b-	2.28E-08	-0.283	0.050	-5.706
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64370	P4:3158	NK Activating 2	16+56	16+56/335+158a-158b-	1.27E-08	-0.274	0.047	-5.817
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64370	P4:3158	NK Activating 2	16+56	16+56/335+158a-158b-	8.59E-07	-0.208	0.041	-5.018
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64370	P4:3158	NK Activating 2	16+56	16+56/335+158a-158b-	6.07E-07	0.200	0.039	5.084
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64370	P4:3158	NK Activating 2	16+56	16+56/335+158a-158b-	1.07E-06	0.202	0.041	4.965
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64370	P4:3158	NK Activating 2	16+56	16+56/335+158a-158b-	1.03E-07	0.219	0.040	5.444
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64371	P4:3159	NK Activating 2	16+56	16+56/CD2+335+158a-158b-	7.27E-07	-0.252	0.050	-5.043
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64371	P4:3159	NK Activating 2	16+56	16+56/CD2+335+158a-158b-	5.35E-07	-0.244	0.048	-5.115
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64371	P4:3159	NK Activating 2	16+56	16+56/CD2+335+158a-158b-	5.96E-07	0.208	0.040	5.130
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64374	P4:3161	NK Activating 2	16+56	16+56/314+335+158a-158b-	6.54E-08	-0.275	0.050	-5.508
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64374	P4:3161	NK Activating 2	16+56	16+56/314+335+158a-158b-	5.23E-08	-0.264	0.048	-5.553
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64374	P4:3161	NK Activating 2	16+56	16+56/314+335+158a-158b-	2.93E-07	0.213	0.041	5.243
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64375	P4:3162	NK Activating 2	16+56	16+56/CD2+314+335+158a-158b-	1.52E-06	-0.245	0.050	-4.887
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64375	P4:3162	NK Activating 2	16+56	16+56/CD2+314+335+158a-158b-	1.36E-06	-0.235	0.048	-4.918
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64375	P4:3162	NK Activating 2	16+56	16+56/CD2+314+335+158a-158b-	8.44E-07	0.205	0.041	5.060
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64431	P4:3212	NK Activating 2	16+56	16+56/335+337-158b-	4.09E-09	-0.284	0.047	-6.015
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64431	P4:3212	NK Activating 2	16+56	16+56/335+337-158b-	2.54E-09	-0.274	0.045	-6.099

IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64431	P4:3212	NK Activating 2	16+56	16+56/335+337-158b-	2.24E-07	-0.207	0.039	-5.277
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64431	P4:3212	NK Activating 2	16+56	16+56/335+337-158b-	1.80E-07	0.199	0.037	5.319
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64431	P4:3212	NK Activating 2	16+56	16+56/335+337-158b-	4.14E-07	0.199	0.039	5.151
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64431	P4:3212	NK Activating 2	16+56	16+56/335+337-158b-	3.60E-08	0.215	0.038	5.632
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64432	P4:3213	NK Activating 2	16+56	16+56/CD2+335+337-158b-	1.89E-07	-0.253	0.048	-5.305
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64432	P4:3213	NK Activating 2	16+56	16+56/CD2+335+337-158b-	1.46E-07	-0.243	0.045	-5.363
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64432	P4:3213	NK Activating 2	16+56	16+56/CD2+335+337-158b-	1.46E-06	0.185	0.038	4.922
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64432	P4:3213	NK Activating 2	16+56	16+56/CD2+335+337-158b-	3.89E-07	0.201	0.039	5.204
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64434	P4:3215	NK Activating 2	16+56	16+56/314+335+337-158b-	1.37E-08	-0.275	0.047	-5.799
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64434	P4:3215	NK Activating 2	16+56	16+56/314+335+337-158b-	1.40E-08	-0.262	0.045	-5.794
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64434	P4:3215	NK Activating 2	16+56	16+56/314+335+337-158b-	7.93E-07	-0.199	0.040	-5.027
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64434	P4:3215	NK Activating 2	16+56	16+56/314+335+337-158b-	9.69E-07	0.188	0.038	4.984
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64434	P4:3215	NK Activating 2	16+56	16+56/314+335+337-158b-	1.61E-07	0.206	0.039	5.348
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64435	P4:3216	NK Activating 2	16+56	16+56/CD2+314+335+337-158b-	3.63E-07	-0.248	0.048	-5.175
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64435	P4:3216	NK Activating 2	16+56	16+56/CD2+314+335+337-158b-	3.74E-07	-0.236	0.046	-5.174
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64435	P4:3216	NK Activating 2	16+56	16+56/CD2+314+335+337-158b-	5.36E-07	0.199	0.039	5.140
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64460	P4:3239	NK Activating 2	16+56	16+56/335+158b-	4.94E-09	-0.283	0.047	-5.982
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64460	P4:3239	NK Activating 2	16+56	16+56/335+158b-	2.97E-09	-0.273	0.045	-6.072
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64460	P4:3239	NK Activating 2	16+56	16+56/335+158b-	2.69E-07	-0.206	0.039	-5.243
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64460	P4:3239	NK Activating 2	16+56	16+56/335+158b-	2.31E-07	0.197	0.037	5.271
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64460	P4:3239	NK Activating 2	16+56	16+56/335+158b-	4.83E-07	0.198	0.039	5.120
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64460	P4:3239	NK Activating 2	16+56	16+56/335+158b-	4.55E-08	0.214	0.038	5.589
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64462	P4:3240	NK Activating 2	16+56	16+56/CD2+335+158b-	2.95E-07	-0.249	0.048	-5.218
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64462	P4:3240	NK Activating 2	16+56	16+56/CD2+335+158b-	2.28E-07	-0.240	0.045	-5.277
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64462	P4:3240	NK Activating 2	16+56	16+56/CD2+335+158b-	5.76E-07	0.198	0.039	5.126
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64464	P4:3242	NK Activating 2	16+56	16+56/314+335+158b-	2.02E-08	-0.272	0.048	-5.727
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64464	P4:3242	NK Activating 2	16+56	16+56/314+335+158b-	2.01E-08	-0.259	0.045	-5.728
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64464	P4:3242	NK Activating 2	16+56	16+56/314+335+158b-	1.16E-06	-0.196	0.040	-4.951
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64464	P4:3242	NK Activating 2	16+56	16+56/314+335+158b-	1.41E-06	0.185	0.038	4.908
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64464	P4:3242	NK Activating 2	16+56	16+56/314+335+158b-	2.28E-07	0.204	0.039	5.282
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64465	P4:3243	NK Activating 2	16+56	16+56/CD2+314+335+158b-	4.83E-07	-0.246	0.048	-5.118
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64465	P4:3243	NK Activating 2	16+56	16+56/CD2+314+335+158b-	4.53E-07	-0.235	0.046	-5.136
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64465	P4:3243	NK Activating 2	16+56	16+56/CD2+314+335+158b-	6.49E-07	0.199	0.039	5.102
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64610	P4:3374	NK Activating 2	16+56	16+56/335+337-158a-	1.18E-06	-0.225	0.045	-4.944
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64641	P4:3401	NK Activating 2	16+56	16+56/335+158a-	1.61E-06	-0.222	0.046	-4.880
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64700	P4:3455	NK Activating 2	16+56	16+56/335+337-	1.14E-06	-0.211	0.043	-4.945
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64730	P4:3482	NK Activating 2	16+56	16+56/335+	1.56E-06	-0.208	0.043	-4.881
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63906	P4:2740	NK Effector	16+56	16+56/335-337-R7-	1.83E-06	0.224	0.046	4.852
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63906	P4:2740	NK Effector	16+56	16+56/335-337-R7-	1.19E-06	0.217	0.044	4.943
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_63935	P4:2767	NK Effector	16+56	16+56/335-R7-	1.60E-06	0.225	0.046	4.880
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_63935	P4:2767	NK Effector	16+56	16+56/335-R7-	1.05E-06	0.218	0.044	4.969
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64084	P4:2900	NK Effector	16+56	16+56/335-337-158a-158b+R7-	1.67E-06	0.246	0.051	4.862
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64084	P4:2900	NK Effector	16+56	16+56/335-337-158a-158b+R7-	9.62E-07	0.219	0.044	4.982
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64084	P4:2900	NK Effector	16+56	16+56/335-337-158a-158b+R7-	8.06E-07	-0.219	0.044	-5.017
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64157	P4:2967	NK Effector	16+56	16+56/335-337-158b+R7-	1.61E-07	0.286	0.054	5.340
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64157	P4:2967	NK Effector	16+56	16+56/335-337-158b+R7-	1.68E-07	0.274	0.051	5.328
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64157	P4:2967	NK Effector	16+56	16+56/335-337-158b+R7-	1.60E-07	0.240	0.045	5.339
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64157	P4:2967	NK Effector	16+56	16+56/335-337-158b+R7-	5.30E-07	-0.225	0.044	-5.104
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64157	P4:2967	NK Effector	16+56	16+56/335-337-158b+R7-	5.31E-07	-0.227	0.045	-5.100
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64157	P4:2967	NK Effector	16+56	16+56/335-337-158b+R7-	8.38E-08	-0.244	0.045	-5.463
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64187	P4:2994	NK Effector	16+56	16+56/335-158b+R7-	1.52E-07	0.287	0.054	5.351
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64187	P4:2994	NK Effector	16+56	16+56/335-158b+R7-	1.58E-07	0.274	0.051	5.339
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64187	P4:2994	NK Effector	16+56	16+56/335-158b+R7-	1.52E-07	0.240	0.045	5.349
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64187	P4:2994	NK Effector	16+56	16+56/335-158b+R7-	5.15E-07	-0.225	0.044	-5.110
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64187	P4:2994	NK Effector	16+56	16+56/335-158b+R7-	5.10E-07	-0.227	0.045	-5.108
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64187	P4:2994	NK Effector	16+56	16+56/335-158b+R7-	8.11E-08	-0.244	0.045	-5.470
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64680	P4:3437	NK Effector	16+56	16+56/335-337-	1.80E-06	0.207	0.043	4.851
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64710	P4:3464	NK Effector	16+56	16+56/335-	1.68E-06	0.207	0.043	4.866
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64950	P4:3680	NK Effector	16+56	16+56/335-337-158b+	1.54E-07	0.286	0.054	5.349
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64950	P4:3680	NK Effector	16+56	16+56/335-337-158b+	1.58E-07	0.274	0.051	5.340
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64950	P4:3680	NK Effector	16+56	16+56/335-337-158b+	1.47E-07	0.240	0.045	5.356
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64950	P4:3680	NK Effector	16+56	16+56/335-337-158b+	4.96E-07	-0.226	0.044	-5.118
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64950	P4:3680	NK Effector	16+56	16+56/335-337-158b+	4.98E-07	-0.228	0.045	-5.112
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64950	P4:3680	NK Effector	16+56	16+56/335-337-158b+	7.72E-08	-0.244	0.045	-5.479
IGP2	The percentage of A2 glycan in total IgG glycans	immuno_64980	P4:3707	NK Effector	16+56	16+56/335-158b+	1.51E-07	0.287	0.054	5.353

IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	immuno_64980	P4:3707	NK Effector	16+56	16+56/335-158b+	1.54E-07	0.275	0.051	5.345
IGP46	The percentage of A2G1 glycan in total Ineutral IgG glycans (GPn)	immuno_64980	P4:3707	NK Effector	16+56	16+56/335-158b+	1.42E-07	0.240	0.045	5.362
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	immuno_64980	P4:3707	NK Effector	16+56	16+56/335-158b+	4.85E-07	-0.226	0.044	-5.122
IGP59	The percentage of fucosylation of agalactosylated structures	immuno_64980	P4:3707	NK Effector	16+56	16+56/335-158b+	4.90E-07	-0.228	0.045	-5.116
IGP60	The percentage of fucosylation of monogalactosylated structures	immuno_64980	P4:3707	NK Effector	16+56	16+56/335-158b+	7.54E-08	-0.244	0.045	-5.483

Table S3: Associations of 51 immune cell traits with AITD and TPOAb level in the TwinsUK cohort

					AITD				TPOAb level			
immuneTrait ID	Trait ID	Canonical name	Lineage	Subset name	Pvalue	Beta	SE	Zscore	Pvalue	Beta	SE	Zscore
immuno_64464	P4:3242	NK Activating 2	16+56	16+56/314+335+158b-	0.043	-0.049	0.024	-2.060	0.768	0.000	0.001	-0.297
immuno_63707	P4:2561	NK Activating 2	16+56	16+56/314+335+158b-R7-	0.045	-0.049	0.024	-2.041	0.769	0.000	0.001	-0.296
immuno_64374	P4:3161	NK Activating 2	16+56	16+56/314+335+158a-158b-	0.049	-0.046	0.023	-1.998	0.709	0.000	0.001	-0.377
immuno_63625	P4:2488	NK Activating 2	16+56	16+56/314+335+158a-158b-R7-	0.050	-0.046	0.023	-1.990	0.723	0.000	0.001	-0.357
immuno_64434	P4:3215	NK Activating 2	16+56	16+56/314+335+337-158b-	0.051	-0.047	0.024	-1.986	0.850	0.000	0.001	-0.191
immuno_63677	P4:2534	NK Activating 2	16+56	16+56/314+335+337-158b-R7-	0.051	-0.047	0.024	-1.985	0.817	0.000	0.001	-0.233
immuno_63703	P4:2558	NK Activating 2	16+56	16+56/335+158b-R7-	0.051	-0.048	0.024	-1.980	0.949	0.000	0.001	-0.065
immuno_64460	P4:3239	NK Activating 2	16+56	16+56/335+158b-	0.052	-0.047	0.024	-1.969	0.951	0.000	0.001	-0.062
immuno_64344	P4:3134	NK Activating 2	16+56	16+56/314+335+337-158a-158b-	0.055	-0.045	0.023	-1.951	0.756	0.000	0.001	-0.314
immuno_63597	P4:2462	NK Activating 2	16+56	16+56/314+335+337-158a-158b-R7-	0.056	-0.045	0.023	-1.945	0.753	0.000	0.001	-0.317
immuno_63674	P4:2531	NK Activating 2	16+56	16+56/335+337-158b-R7-	0.057	-0.047	0.024	-1.930	0.994	0.000	0.001	-0.008
immuno_64431	P4:3212	NK Activating 2	16+56	16+56/335+337-158b-	0.059	-0.046	0.024	-1.914	0.984	0.000	0.001	0.021
immuno_64370	P4:3158	NK Activating 2	16+56	16+56/335+158a-158b-	0.065	-0.044	0.023	-1.870	0.851	0.000	0.001	-0.190
immuno_63595	P4:2460	NK Activating 2	16+56	16+56/335+337-158a-158b-R7-	0.066	-0.044	0.023	-1.867	0.925	0.000	0.001	-0.095
immuno_63622	P4:2485	NK Activating 2	16+56	16+56/335+158a-158b-R7-	0.066	-0.044	0.023	-1.865	0.844	0.000	0.001	-0.198
immuno_64341	P4:3131	NK Activating 2	16+56	16+56/335+337-158a-158b-	0.072	-0.043	0.023	-1.826	0.945	0.000	0.001	-0.070
immuno_64641	P4:3401	NK Activating 2	16+56	16+56/335+158a-	0.086	-0.041	0.024	-1.729	0.750	0.000	0.001	0.324
immuno_63906	P4:2740	NK Effector	16+56	16+56/335-337-R7-	0.086	0.043	0.025	1.726	0.351	0.000	0.001	-0.954
immuno_64680	P4:3437	NK Effector	16+56	16+56/335-337-	0.087	0.043	0.025	1.727	0.365	0.000	0.001	-0.926
immuno_63935	P4:2767	NK Effector	16+56	16+56/335-R7-	0.087	0.043	0.025	1.720	0.335	-0.001	0.001	-0.987
immuno_64730	P4:3482	NK Activating 2	16+56	16+56/335+	0.088	-0.043	0.025	-1.719	0.358	0.000	0.001	0.941
immuno_64710	P4:3464	NK Effector	16+56	16+56/335-	0.088	0.043	0.025	1.718	0.355	0.000	0.001	-0.947
immuno_64610	P4:3374	NK Activating 2	16+56	16+56/335+337-158a-	0.094	-0.040	0.024	-1.688	0.701	0.000	0.001	0.389
immuno_63835	P4:2677	NK Activating 2	16+56	16+56/335+337-158a-R7-	0.096	-0.040	0.024	-1.675	0.710	0.000	0.001	0.378
immuno_64700	P4:3455	NK Activating 2	16+56	16+56/335+337-	0.104	-0.041	0.025	-1.637	0.313	0.001	0.001	1.035
immuno_63925	P4:2758	NK Activating 2	16+56	16+56/335+337-R7-	0.104	-0.041	0.025	-1.636	0.322	0.001	0.001	1.016
immuno_64465	P4:3243	NK Activating 2	16+56	16+56/CD2+314+335+158b-	0.153	-0.033	0.023	-1.443	0.988	0.000	0.001	-0.016
immuno_63708	P4:2562	NK Activating 2	16+56	16+56/CD2+314+335+158b-R7-	0.155	-0.033	0.023	-1.434	0.995	0.000	0.001	0.006
immuno_64375	P4:3162	NK Activating 2	16+56	16+56/CD2+314+335+158a-158b-	0.161	-0.032	0.023	-1.414	0.838	0.000	0.001	-0.211
immuno_63626	P4:2489	NK Activating 2	16+56	16+56/CD2+314+335+158a-158b-R7-	0.162	-0.032	0.023	-1.410	0.855	0.000	0.001	-0.188
immuno_64435	P4:3216	NK Activating 2	16+56	16+56/CD2+314+335+337-158b-	0.164	-0.033	0.023	-1.404	0.916	0.000	0.001	0.109
immuno_63678	P4:2535	NK Activating 2	16+56	16+56/CD2+314+335+337-158b-R7-	0.165	-0.033	0.023	-1.400	0.896	0.000	0.001	0.135
immuno_62860	P4:18	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-R7-	0.175	-0.031	0.023	-1.368	0.963	0.000	0.001	-0.048
immuno_63623	P4:2486	NK Activating 2	16+56	16+56/CD2+335+158a-158b-R7-	0.178	-0.031	0.023	-1.358	0.875	0.000	0.001	-0.162
immuno_63704	P4:2559	NK Activating 2	16+56	16+56/CD2+335+158b-R7-	0.179	-0.032	0.024	-1.354	0.939	0.000	0.001	0.079
immuno_64371	P4:3159	NK Activating 2	16+56	16+56/CD2+335+158a-158b-	0.179	-0.031	0.023	-1.356	0.856	0.000	0.001	-0.187
immuno_64462	P4:3240	NK Activating 2	16+56	16+56/CD2+335+158b-	0.180	-0.032	0.024	-1.354	0.940	0.000	0.001	0.078
immuno_64345	P4:3135	NK Activating 2	16+56	16+56/CD2+314+335+337-158a-158b-	0.180	-0.031	0.023	-1.351	0.923	0.000	0.001	-0.100
immuno_63675	P4:2532	NK Activating 2	16+56	16+56/CD2+335+337-158b-R7-	0.189	-0.031	0.024	-1.323	0.864	0.000	0.001	0.177
immuno_64432	P4:3213	NK Activating 2	16+56	16+56/CD2+335+337-158b-	0.189	-0.031	0.024	-1.326	0.896	0.000	0.001	0.135
immuno_64342	P4:3132	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-	0.197	-0.030	0.023	-1.300	0.981	0.000	0.001	-0.024
immuno_63596	P4:2461	NK Activating 2	16+56	16+56/CD2+335+337-158a-158b-R7-	0.202	-0.030	0.023	-1.286	0.978	0.000	0.001	-0.028
immuno_64157	P4:2967	NK Effector	16+56	16+56/335-337-158b+R7-	0.805	0.006	0.023	0.248	0.464	-0.001	0.001	-0.758
immuno_64187	P4:2994	NK Effector	16+56	16+56/335-158b+R7-	0.808	0.006	0.023	0.244	0.466	-0.001	0.001	-0.754
immuno_64980	P4:3707	NK Effector	16+56	16+56/335-158b+	0.816	0.005	0.023	0.233	0.459	-0.001	0.001	-0.765
immuno_64950	P4:3680	NK Effector	16+56	16+56/335-337-158b+	0.816	0.005	0.023	0.233	0.457	-0.001	0.001	-0.769
immuno_64161	P4:2970	NK Activating 1	16+56	16+56/314+335-337-158b+R7-	0.893	0.003	0.023	0.135	0.454	-0.001	0.001	-0.778
immuno_64953	P4:3683	NK Activating 1	16+56	16+56/314+335-337-158b+	0.896	0.003	0.023	0.130	0.453	-0.001	0.001	-0.778
immuno_64190	P4:2997	NK Activating 1	16+56	16+56/314+335-158b+R7-	0.904	0.003	0.023	0.121	0.453	-0.001	0.001	-0.780
immuno_64984	P4:3710	NK Activating 1	16+56	16+56/314+335-158b+	0.905	0.003	0.023	0.120	0.453	-0.001	0.001	-0.778
immuno_64084	P4:2900	NK Effector	16+56	16+56/335-337-158a-158b+R7-	0.970	0.001	0.024	0.038	0.528	-0.001	0.001	-0.648

Table S4: Hits from selected eQTL studies for two SNPs, rs1521 and rs3094228 in the thyroid cells and whole blood

* GWAS catalog for the genetic variants associated with thyroid phenotypes(Data downloaded from GWAS Catalog on 17/06/2015)

** eQTLs from Haploreg v4.1 (https://pubs.broadinstitute.org/mammals/haploreg/haploreg.php) and GTEx v6,v7, v8 (https://www.gtexportal.org/home/)

Lead SNP-risk allele	Thyroid phenotypes (from GWAS catalog)* Chromosom	start (hg38)	end (hg38)	Phenotype	eQTL** Study ID	Paper Title	PMID	ref allele	Tissue	Correlated gene		NES	p-value
rs1521-T	6	31382927	31382927	Graves' disease	GTEx2019_v8 (dbGaP Accession phs000424.v8.p2)	The GTEx Consortium atlas of genetic regulatory effects across human tissues	i.org/10.110'	C	Thyroid	VARS2	ENSG00000137411.16	0.29	5.00E-12
									Thyroid	MIR6891	ENSG00000277402.1	0.35	6.20E-11
									Thyroid	HCG27	ENSG00000206344.7	0.21	1.40E-09
									Thyroid	**HLA-C**	ENSG00000204525.16	-0.24	8.20E-08
									Thyroid	PSORS1C3	ENSG00000204528.3	0.33	7.50E-08
									Thyroid	XXbac-BPG181B23.7	ENSG00000272221.1	-0.25	1.40E-06
									Thyroid	**MICA**	ENSG00000204520.12	-0.18	2.50E-05
									Thyroid	PRRT1	ENSG00000204314.10	0.12	4.20E-05
									Thyroid	FLOT1	ENSG00000137312.14	0.11	6.50E-05
									Whole_Blood	XXbac-BPG181B23.7	ENSG00000272221.1	-0.34	2.20E-17
									Whole_Blood	MIR6891	ENSG00000277402.1	0.28	1.40E-09
									Whole_Blood	PSORS1C3	ENSG00000204528.3	0.21	2.30E-08
									Whole_Blood	XXbac-BPG299F13.17	ENSG00000272501.1	-0.12	2.20E-07
									Whole_Blood	HCG27	ENSG00000206344.7	0.088	1.20E-05
									Whole_Blood	VARS2	ENSG00000137411.16	0.1	2.20E-05
									Whole_Blood	DDR1	ENSG00000204580.13	0.17	2.80E-05
									Whole_Blood	ZBTB12	ENSG00000204366.3	0.2	3.20E-05
									Whole_Blood	**HLA-C**	ENSG00000204525.16	-0.12	5.70E-05
									Whole_Blood	C4A	ENSG00000244731.7	-0.2	1.30E-04
									Whole_Blood	FLOT1	ENSG00000137312.14	0.045	1.70E-04
					GTEx2017_v7 (dbGaP Accession phs000424.v7.p2)	ıe Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in huma	29022597	C	Thyroid	VARS2	ENSG00000137411.12	0.31	3.40E-09
									Thyroid	HCG27	ENSG00000206344.6	0.23	6.90E-08
									Thyroid	**HLA-C**	ENSG00000204525.10	-0.25	8.30E-06
									Thyroid	PSORS1C3	ENSG00000204528.3	0.31	2.00E-05
									Whole_Blood	XXbac-BPG181B23.7	ENSG00000272221.1	-0.33	7.90E-08
									Thyroid	**HLA-C**	ENSG00000204525.10	NA	1.28E-08
					GTEx2015_v6	ıe Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in huma	25954001	C	Thyroid	XXbac-BPG248L24.12		NA	1.03E-08
									Whole_Blood	**HLA-C**	ENSG00000204525.10	NA	2.98E-08
									Whole_Blood	XXbac-BPG181B23.7	ENSG00000272221.1	NA	2.86E-07
									Whole_Blood	XXbac-BPG248L24.12		NA	8.29E-09
									Whole_Blood	-		NA	1.11E-35
									Whole_Blood	-		NA	6.64E-38
					Westra2013	Systematic identification of trans eQTLs as putative drivers of known disease associations	24013639		Whole_Blood	AIF1	ENSG00000204472	NA	2.51E-06
									Whole_Blood	ATP6V1G2|BAT1	ENSG00000213760	NA	9.31E-16
									Whole_Blood	**HCP5**	ENSG00000206337.6	NA	4.62E-06
									Whole_Blood	LTA	ENSG00000226979	NA	8.46E-10
									Whole_Blood	**MICB**	ENSG00000204516.5	NA	5.24E-04
rs3094228-C	6	31462150	31462150	Thyroid peroxidase antibody positivity (TPOAb-positivity)	GTEx2019_v8 (dbGaP Accession phs000424.v8.p2)	The GTEx Consortium atlas of genetic regulatory effects across human tissues	i.org/10.110'	T	Thyroid	C4A	ENSG00000244731.7	-0.39	2.00E-16
									Thyroid	CYP21A1P	ENSG00000204338.8	-0.37	2.80E-14
									Thyroid	**MICB**	ENSG00000204516.9	0.26	3.70E-09
									Thyroid	**HCP5**	ENSG00000206337.10	-0.24	3.00E-08
									Thyroid	FLOT1	ENSG00000137312.14	0.17	5.00E-08
									Thyroid	PSORS1C1	ENSG00000204540.10	-0.37	7.00E-08
									Thyroid	CCHCR1	ENSG00000204536.13	0.2	2.00E-07
									Thyroid	**HLA-C**	ENSG00000204525.16	0.25	9.30E-07
									Thyroid	HLA-S	ENSG00000225851.1	-0.31	3.80E-06
									Thyroid	RNF5	ENSG00000204308.7	-0.14	2.70E-05
									Whole_Blood	C4A	ENSG00000244731.7	-0.48	1.50E-16
									Whole_Blood	C4B	ENSG00000224389.8	0.47	2.60E-13
									Whole_Blood	CYP21A1P	ENSG00000204338.8	-0.4	1.10E-12
									Whole_Blood	CYP21A2	ENSG00000231852.6	0.4	3.20E-10
									Whole_Blood	FLOT1	ENSG00000137312.14	0.058	2.20E-05
									Whole_Blood	HLA-S	ENSG00000225851.1	-0.27	3.70E-05
									Whole_Blood	CCHCR1	ENSG00000204536.13	0.13	8.10E-05
									Whole_Blood	XXbac-BPG248L24.12	ENSG00000271581.1	-0.24	1.50E-04
									Thyroid	C4A	ENSG00000244731.3	-0.4	3.40E-13
									Thyroid	CYP21A1P	ENSG00000204338.4	-0.37	1.10E-09
									Thyroid	**HCP5**	ENSG00000206337.6	-0.32	1.30E-09
									Thyroid	PSORS1C1	ENSG00000204540.6	-0.4	4.00E-06
					GTEx2017_v7 (dbGaP Accession phs000424.v7.p2)	ıe Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in huma	29022597	T	Thyroid	HCG22	ENSG00000228789.2	-0.35	5.10E-06
									Thyroid	**MICB**	ENSG00000204516.5	0.26	5.10E-06
									Thyroid	CCHCR1	ENSG00000204536.9	0.21	1.70E-05
									Whole_Blood	C4A	ENSG00000244731.3	-0.48	4.00E-09
									Whole_Blood	CYP21A1P	ENSG00000204338.4	-0.41	3.80E-07
									Whole_Blood	C4B	ENSG00000224389.4	0.41	9.90E-06
									Whole_Blood	CYP21A2	ENSG00000231852.2	0.38	2.90E-05
rs2596460	6	31449483	31449483	16+56/CD2-314+335-337-158a+158b+	GTEx2019_v8 (dbGaP Accession phs000424.v8.p2)	The GTEx Consortium atlas of genetic regulatory effects across human tissues	https://doi.org/10.1101/787903	A	Thyroid	ATP6V1G2	ENSG00000213760.10	0.28	1.10E-05
									Thyroid	SKIV2L	ENSG00000204351.11	0.23	2.20E-05
									Thyroid	CCHCR1	ENSG00000204536.13	-0.22	1.30E-04
									Thyroid	VARS2	ENSG00000137411.16	-0.27	2.00E-04
									Whole_Blood	**MICA**	ENSG00000204520.12	0.22	3.40E-04
					GTEx2017_v7 (dbGaP Accession phs000424.v7.p2)	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans	29022597		**Whole_Blood**	**HLA-C**	ENSG00000204525.10	-0.3	5.60E-05
									Thyroid	CCHCR1	ENSG00000204536.9	-0.29	2.40E-05
rs2596457	6	31449995	31449995	16+56/CD2-314+335-337-158a+158b+	GTEx2019_v8 (dbGaP Accession phs000424.v8.p2)	The GTEx Consortium atlas of genetic regulatory effects across human tissues	https://doi.org/10.1101/787903	A	Thyroid	ATP6V1G2	ENSG00000213760.10	0.3	2.10E-06
									Thyroid	SKIV2L	ENSG00000204351.11	0.24	8.70E-06
									Thyroid	VARS2	ENSG00000137411.16	-0.28	1.70E-04
									Thyroid	CCHCR1	ENSG00000204536.13	-0.21	2.70E-04
									Thyroid	DDR1	ENSG00000204580.13	-0.18	4.60E-04
									Whole blood	**MICA**	ENSG00000204520.12	0.22	2.40E-04
					GTEx2017_v7 (dbGaP Accession phs000424.v7.p2)	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans	29022597		Thyroid	ATP6V1G2	ENSG00000213760.6	0.31	3.60E-05
									Thyroid	CCHCR1	ENSG00000204536.9	-0.28	4.80E-05
rs2523691	6	31452660	31452660	16+56/CD2-314+335-337-158a+158b+	GTEx2019_v8 (dbGaP Accession phs000424.v8.p2)	The GTEx Consortium atlas of genetic regulatory effects across human tissues	https://doi.org/10.1101/787903	G	Thyroid	ATP6V1G2	ENSG00000213760.10	0.28	1.10E-05
									Thyroid	SKIV2L	ENSG00000204351.11	0.23	2.20E-05
									Thyroid	CCHCR1	ENSG00000204536.13	-0.22	1.30E-04
									Thyroid	VARS2	ENSG00000137411.16	-0.27	2.00E-04
									Whole_Blood	**MICA**	ENSG00000204520.12	0.22	3.40E-04
					GTEx2017_v7 (dbGaP Accession phs000424.v7.p2)	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans	29022597		**Whole_Blood**	**HLA-C**	ENSG00000204525.10	-0.3	5.50E-05
									Thyroid	CCHCR1	ENSG00000204536.9	-0.29	1.90E-05

Table S5 : Genes reported for genetic variants associated with thyroid phenotypes and immune cell traits

* the closest genes reported in GWAS catalog for the genetic variants associated with thyroid phenotypes and immune cell traits (Data downloaded from GWAS Catalog on 17/06/2015)

** Roederer, M et al., Cell, 2015, doi: 10.1016/j.cell.2015.02.046 and Mangino et al, Nature Communications, 2017, https://doi.org/10.1038/ncomms13850

Name of gene reported in GWAS catalog* and Roederer's paper **	Thyroid phenotypes (from GWAS catalog)*						LD (r2)	distance lead SNP(thryoid)-lead SNP(immune cell traits)	Immune cell traits**								
	Lead SNP	Chromosome	start (hg38)	end (hg38)	Phenotype	AITD status or biomarkers associated with AITD			Lead SNP	Chromosome	start (hg38)	end (hg38)	start (hg19)	end (hg19)	Immune Name in TwinsUK	Phenotypes	
HCP5	rs3094228	6	31462150	31462150	Thyroid peroxidase antibody positivity	Yes	<0.2	12667	rs2596460	6	31449483	31449483	31449733	31449733	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
							<0.2	12155	rs2596457	6	31449995	31449995	31450245	31450245	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
							<0.2	9490	rs2523691	6	31452660	31452660	31452910	31452910	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
MICA	rs1521	6	31382927	31382927	Graves' disease	Yes	<0.2	-66556	rs2596460	6	31449483	31449483	31449733	31449733	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
ACCN1	rs9901756	17	34137135	34137135	Hypothyroidism	No	<0.2	365816	rs12603968	17	33771319	33771319	33771319	33771319	P4:3551	NK Effector	16+56/314-158a+
							<0.2	366131	rs12602135	17	33771004	33771004	33771004	33771004	P4:3551	NK Effector	16+56/314-158a+
DIRC3	rs6759952	2	217406996	217406996	Thyroid cancer	No	<0.2	-317240	rs744564	2	217724236	217724236	217724236	217724236	P4:3551	NK Effector	16+56/314-158a+
	rs966423	2	217445617	217445617			<0.2	-278619									
GLIS3	rs1571583	9	4267209	4267209	Thyroid hormone levels	No	<0.2	492850	rs10973456	9	3774359	3774359	3774359	3774359	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
HACE1	rs9322817	6	104784358	104784358	Thyroid stimulating hormone level	No	<0.2	378569	rs156205	6	104405789	104405789	104405789	104405789	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
L3MBTL4	rs948426	18	6567183	6567183	Hypothyroidism	No	<0.2	438743	rs17486103	18	6128440	6128440	6128440	6128440	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
NFIA	rs334699	1	61154824	61154824	Thyroid hormone levels	No	<0.2	-240528	rs11581697	1	61395352	61395352	61395352	61395352	P4:3551	NK Effector	16+56/314-158a+
							<0.2	-240632	rs12072379	1	61395456	61395456	61395456	61395456	P4:3551	NK Effector	16+56/314-158a+
NFIB	rs10961534	9	14470835	14470835	Hypothyroidism	No	<0.2	31760	rs11787815	9	14439075	14439075	14439075	14439075	P4:3551	NK Effector	16+56/314-158a+
NR3C2	rs10028213	4	148731458	148731458	Thyroid stimulating hormone level	No	<0.2	441933	rs3910047	4	148289525	148289525	148289525	148289525	P4:3551	NK Effector	16+56/314-158a+
NRG1	rs7825175	8	32558756	32558756	Thyroid hormone levels	No	<0.2	5271541	rs4279551	8	27287215	27287215	27287215	27287215	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
							<0.2	510838	rs2881470	8	32047918	32047918	32047918	32047918	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
							<0.2	488634	rs1462900	8	32070122	32070122	32070122	32070122	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
							<0.2	480970	rs1381871	8	32077786	32077786	32077786	32077786	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
							<0.2	496755	rs1471387	8	32078096	32078096	32078096	32078096	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
	rs2439302	8	32574851	32574851	Thyroid cancer	No	<0.2	494464	rs1947734	8	32080387	32080387	32080387	32080387	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
							<0.2	488995	rs7818326	8	32085856	32085856	32085856	32085856	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
							<0.2	488541	rs16878780	8	32086310	32086310	32086310	32086310	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
							<0.2	488339	rs9297185	8	32086512	32086512	32086512	32086512	P7:110	DC mDC imDC	11c+ (nodim)/1c-/16+/32+
PDE10A	rs753760	6	165632995	165632995	Thyroid hormone levels	No	<0.2	152041	rs551901	6	165480954	165480954	165480954	165480954	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
							<0.2	151764	rs684847	6	165481231	165481231	165481231	165481231	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
SOX9	rs9915657	17	72131395	72131395	Thyroid hormone levels	No	<0.2	691727	rs9302936	17	71439668	71439668	71439668	71439668	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
							<0.2	686259	rs1990222	17	71445136	71445136	71445136	71445136	P4:3763	NK Activating 1	16+56/CD2-314+335-337-158a+158b+
VAV3	rs12126655	1	107814198	107814198	Plasma thyroid-stimulating hormone levels	No	<0.2	-121433	rs10494086	1	107935631	107935631	107935631	107935631	P4:3551	NK Effector	16+56/314-158a+
							<0.2	-127812	rs1020812	1	107942010	107942010	107942010	107942010	P4:3551	NK Effector	16+56/314-158a+
	rs4915077	1	107823394	107823394	Hypothyroidism	No	<0.2	-123692	rs6696531	1	107947086	107947086	107947086	107947086	P4:3551	NK Effector	16+56/314-158a+

Table S6: Glycome-wide associations studies of 17 AITD-IgG N-glycan traits with 1,113 circulating proteins. Only significant ones were put here.

Glycan ID	Description	Soma ID	Target	Uniprot	P-value	Beta	SE
IGP2	The percentage of A2 glycan in total IgG glycans	SL008609	FCG3B	O75015	1.46E-06	0.051	0.010
IGP8	The percentage of FA2[3]G1 glycan in total IgG glycans	SL007464	AMHR2	Q16671	1.50E-07	0.029	0.005
IGP8	The percentage of FA2[3]G1 glycan in total IgG glycans	SL004857	Desmoglein-2	Q14126	2.15E-06	0.032	0.007
IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	SL008609	FCG3B	O75015	2.63E-06	0.050	0.010
IGP46	The percentage of A2G1 glycan in total lneutral IgG glycans (GPn)	SL008609	FCG3B	O75015	3.88E-06	0.045	0.009
IGP48	The percentage of FA2[3]G1 glycan in total neutral IgG glycans (GPn)	SL002644	ERBB1	P00533	3.04E-06	0.023	0.005
IGP48	The percentage of FA2[3]G1 glycan in total neutral IgG glycans (GPn)	SL000283	b2-Microglobulin	P61769	4.16E-06	-0.034	0.007
IGP56	The percentage of monogalactosylated structures in total neutral IgG glycans	SL000283	b2-Microglobulin	P61769	5.10E-07	-0.037	0.007
IGP57	The percentage of digalactosylated structures in total neutral IgG glycans	SL004159	TRAIL R4	Q9UBN6	2.95E-06	-0.041	0.008
IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	SL008609	FCG3B	O75015	5.21E-06	-0.044	0.009
IGP59	The percentage of fucosylation of agalactosylated structures	SL008609	FCG3B	O75015	9.33E-06	-0.044	0.010
IGP60	The percentage of fucosylation of monogalactosylated structures	SL008609	FCG3B	O75015	4.06E-07	-0.048	0.009
IGP62	The percentage of fucosylated (without bisecting GlcNAc) structures in total neutral IgG glycans	SL004672	BCMA	Q02223	5.44E-08	0.041	0.007
IGP63	The percentage of fucosylation (without bisecting GlcNAc) of agalactosylated structures	SL004672	BCMA	Q02223	1.47E-07	0.041	0.007
IGP63	The percentage of fucosylation (without bisecting GlcNAc) of agalactosylated structures	SL004857	Desmoglein-2	Q14126	8.02E-06	0.032	0.007

Table S7: Genetic variants associated with thyroid phenotypes and AITD-IgG N-glycan traits overlapping pQTL identified in INTERVAL project (LD r2>0.8)
*Sun et al, Nature, 2018, doi: 10.1038/s41586-018-0175-2

GWAS Catalog (Data downloaded from GWAS Catalog on 17/06/2015)											pQTL*							
chr	Start (hg38)	Stop (hg38)	Strongest SNPs	SNPs	Disease traits	Region	Reported Genes	Mapped Genes	Context	Extra Information about GWAS findings	SOMAmer ID (version 2) used here	SOMAmer ID (version 4)	Target	Target fullname	UniProt	*cis/ trans*	Mapped gene	Sentinel variant	LD with sentinel variant (r2)
1	157699488	157699488	rs3761959-A, rs3761959-G	rs3761959	**Graves disease**, Multiple sclerosis	1q23.1	FCRL3	FCRL3	intron		SL014088	FCRL3.4440.15.2	FCRL3	Fc receptor-like protein 3	Q96P31	cis	FCRL3	rs7528684	1
1	157701026	157701026	rs7528684-T	rs7528684	Type 1 diabetes autoantibodies, Rheumatoid arthritis, **Graves disease**	1q23.1	FCRL3	FCRL3	nearGene-5	I-A2A									
9	133273813	133273813	rs505922-C, rs505922-T, rs505922-?	rs505922	Protein quantitative trait loci, Venous thromboembolism, End-stage coagulation, Pancreatic cancer, **Graves disease**, Duodenal ulcer	9q34.2	ABO	ABO	intron	Recessive, TNFA, vWF	No detected	DHFR.9823.2.3	DYR	Dihydrofolate reductase	P00374	*trans*	*ABO*	rs676457	0.99
											SL004516	MBL2.3000.66.1	MBL	Mannose-binding protein C	P11226	*trans*	*ABO*	rs139840563	0.98
											No detected	ABO.9253.52.3	BGAT	Histo-blood group ABO system transferase	P16442	*cis*	*ABO*	rs505922	1
											SL004857	DSG2.9484.75.3	Desmoglein-2	Desmoglein-2	Q14126	*trans*	*ABO*	rs687621	0.97
											SL005157	CD209.3029.52.2	DC-SIGN	CD209 antigen	Q9NNX6	*trans*	*ABO*	rs505922	1
											No detected	CHST11.7779.86.3	CHSTB	Carbohydrate sulfotransferase 11	Q9NPF2	*trans*	*ABO*	rs687621	0.97
12	111446804	111446804	rs3184504-C, rs3184504-?, rs3184504-T	rs3184504	Type 1 diabetes, Platelet counts, Blood metabolite levels, Beta-2 microglubulin plasma levels, Diastolic blood pressure, Coronary artery disease, Eosinophil counts, Systolic blood pressure, Autoimmune hepatitis type-1, Red blood cell traits, Rheumatoid arthritis, Type 1 diabetes autoantibodies, **Hypothyroidism**, Coronary heart disease	12q24.12	SH2B3, NAA25, C12orf51, ATXN2, BRAP, LOC100101246, PTPN11	SH2B3	missense	T1D, kynurenine, Hgb, EA	SL006460	GP1BA.4990.87.1	GP1BA	Platelet glycoprotein Ib alpha chain	P07359	*trans*	*BRAP*	rs11065979	0.81
												VCAM1.2967.8.1	VCAM-1	Vascular cell adhesion protein 1	P19320	*trans*	*SH2B3*	rs3184504	1

Table S8: Heritability of AITD, 17 IgG N-glycan traits and 51 immune cell traits in the TwinsUK cohort

* Martin et al, 2018

** Mangino et al, Nature Communications, 2017, https://doi.org/10.1038/ncomms13850

type	features	general info	best model	H2 [95%CI]	A [95%CI]	D [95%CI]	C [95%CI]	E [95%CI]
thyroid phenotype*	AITD		DE	0.63 [0.59-0.67]	NS	0.63 [0.59-0.67]	NS	0.36 [0.32-0.40]
	TPOAb-positivity		DE	0.57 [0.50-0.65]	NS	0.57 [0.50-0.65]	NS	0.42 [0.34-0.49]
IgG N-glycan traits*	IGP2	The percentage of A2 glycan in total IgG glycans	AE	0.731 [0.747;0.716]	0.731 [0.697;0.764]	NS	NS	0.269 [0.236;0.303]
	IGP7	The percentage of FA2[6]G1 glycan in total IgG glycans	AE	0.557 [0.563;0.552]	0.557 [0.509;0.605]	NS	NS	0.443 [0.395;0.491]
	IGP8	The percentage of FA2[3]G1 glycan in total IgG glycans	AE	0.662 [0.676;0.65]	0.662 [0.621;0.702]	NS	NS	0.338 [0.298;0.379]
	IGP15	The percentage of FA2G1S1 glycan in total IgG glycans	AE	0.704 [0.72;0.691]	0.704 [0.669;0.739]	NS	NS	0.296 [0.261;0.331]
	IGP21	The percentage of A2BG2S2 glycan in total IgG glycans	AE	0.347 [0.327;0.363]	0.347 [0.288;0.406]	NS	NS	0.653 [0.594;0.712]
	IGP33	Ratio of all fucosylated (+/- bisecting GlyNAc) monosialylated and disialylated structures in total IgG glycans	DCE	0.241 [0.183;0.277]	NS	0.241 [0.142;0.34]	0.246 [0.175;0.316]	0.513 [0.457;0.57]
	IGP36	Ratio of all fucosylated sialylated structures with and without bisecting GlcNAc	AE	0.704 [0.72;0.691]	0.704 [0.669;0.739]	NS	NS	0.296 [0.261;0.331]
	IGP42	The percentage of A2 glycan in total neutral IgG glycans (GPn)	AE	0.739 [0.755;0.724]	0.739 [0.706;0.771]	NS	NS	0.261 [0.229;0.294]
	IGP45	*The percentage of FA2B glycan in total neutral IgG glycans (GP^n)*	DCE	0.41 [0.407;0.413]	NS	0.41 [0.346;0.475]	0.361 [0.305;0.416]	0.229 [0.199;0.259]
	IGP46	*The percentage of A2G1 glycan in total Ineutral IgG glycans (GP^n)*	AE	0.725 [0.742;0.711]	0.725 [0.691;0.76]	NS	NS	0.275 [0.24;0.309]
	IGP48	The percentage of FA2[3]G1 glycan in total neutral IgG glycans (GPn)	AE	0.776 [0.793;0.761]	0.776 [0.747;0.805]	NS	NS	0.224 [0.195;0.253]
	IGP56	The percentage of monogalactosylated structures in total neutral IgG glycans	ADE	0.678 [0.492;0.749]	0.475 [0.277;0.674]	0.203 [0;0.411]	NS	0.322 [0.281;0.363]
	IGP58	The percentage of all fucosylated (+/- bisecting GlcNAc) structures in total neutral IgG glycans	DCE	0.57 [0.599;0.55]	NS	0.57 [0.494;0.646]	0.162 [0.098;0.226]	0.268 [0.232;0.303]
	IGP59	*The percentage of fucosylation of agalactosylated structures*	ADE	0.735 [0.591;0.791]	0.333 [0.136;0.531]	0.401 [0.197;0.605]	NS	0.265 [0.231;0.3]
	IGP60	*The percentage of fucosylation of monogalactosylated structures*	AE	0.714 [0.731;0.7]	0.714 [0.677;0.751]	NS	NS	0.286 [0.249;0.323]
	IGP62	*The percentage of fucosylated (without bisecting GlcNAc) structures in total neutral IgG glycans*	AE	0.76 [0.777;0.745]	0.76 [0.729;0.79]	NS	NS	0.24 [0.21;0.271]
	IGP63	*The percentage of fucosylation (without bisecting GlcNAc) of agalactosylated structures*	AE	0.737 [0.754;0.722]	0.737 [0.703;0.771]	NS	NS	0.263 [0.229;0.297]
immnune cell traits**	P4:3242	16+56/314+335+158b-	ACE	0.427 [0.20;0.66]	0.427 [0.20;0.66]	NS	0.356[0.14;0.54]	0.217 [0.16;0.31]
	P4:2561	16+56/314+335+158b-R7-	ACE	0.424 [0.19;0.66]	0.424 [0.19;0.66]	NS	0.358 [0.14;0.54]	0.218 [0.16;0.31]
	P4:3161	16+56/314+335+158a-158b-	AE	0.792 [0.71;0.81]	0.792 [0.71;0.81]	NS	NS	0.208 [015;0.29]
	P4:2488	16+56/314+335+158a-158b-R7-	AE	0.792 [0.71;0.81]	0.792 [0.71;0.81]	NS	NS	0.208 [015;0.29]
	P4:3215	16+56/314+335+337-158b-	ACE	0.422 [0.19;0.66]	0.422 [0.19;0.66]	NS	0.358 [0.14;0.54]	0.22[0.16;0.31]
	P4:2534	16+56/314+335+337-158b-R7-	ACE	0.423 [0.19;0.66]	0.423 [0.19;0.66]	NS	0.356 [0.14;0.54]	0.221[0.16;0.31]
	P4:2558	16+56/335+158b-R7-	ACE	0.439 [0.21;0.68]	0.439 [0.21;0.68]	NS	0.344 [0.12;0.53]	0.217[0.16;0.31]
	P4:3239	16+56/335+158b-	ACE	0.437 [0.20;0.68]	0.437 [0.20;0.68]	NS	0.344 [0.12;0.53]	0.22[0.16;0.31]
	P4:3134	16+56/314+335+337-158a-158b-	AE	0.791 [0.71;0.85]	0.792 [0.71;0.85]	NS	NS	0.209 [015;0.29]
	P4:2462	16+56/314+335+337-158a-158b-R7-	AE	0.783 [0.70;0.84]	0.783 [0.70;0.84]	NS	NS	0.217 [016;0.30]
	P4:2531	16+56/335+337-158b-R7-	ACE	0.433 [0.20;0.67]	0.433 [0.20;0.67]	NS	0.347 [0.13;0.53]	0.217[0.16;0.31]
	P4:3212	16+56/335+337-158b-	ACE	0.428 [0.19;0.67]	0.428 [0.19;0.67]	NS	0.347[0.12;0.53]	0.225 [0.16;0.32]
	P4:3158	16+56/335+158a-158b-	AE	0.792 [0.71;0.81]	0.792 [0.71;0.81]	NS	NS	0.208 [015;0.29]
	P4:2460	16+56/335+337-158a-158b-R7-	AE	0.782 [0.70;0.84]	0.782 [0.70;0.84]	NS	NS	0.218 [016;0.30]
	P4:2485	16+56/335+158a-158b-R7-	AE	0.783 [0.70;0.84]	0.783 [0.70;0.84]	NS	NS	0.217 [016;0.30]
	P4:3131	16+56/335+337-158a-158b-	AE	0.781 [0.70;0.84]	0.781 [0.70;0.84]	NS	NS	0.219 [016;0.30]
	P4:3401	16+56/335+158a-	ACE	0.475 [0.26;0.70]	0.475 [0.26;0.70]	NS	0.337 [0.12;0.51]	0.188[0.13;0.27]
	P4:2740	16+56/335-337-R7-	ACE	0.349 [0.15;0.55]	0.349 [0.15;0.55]	NS	0.461 [0.27;0.62]	0.19 [0.14;0.27]
	P4:3437	16+56/335-337-	ACE	0.303 [0.11;0.50]	0.303 [0.11;0.50]	NS	0.509 [0.33;0.66]	0.188 [0.13;0.27]
	P4:2767	16+56/335-R7-	ACE	0.352 [0.15;0.56]	0.352 [0.15;0.56]	NS	0.46 [0.27;0.62]	0.188 [0.13;0.27]
	P4:3482	16+56/335+	ACE	0.303 [0.11;0.50]	0.303 [0.11;0.50]	NS	0.51 [0.33;0.66]	0.187[0.13;0.27]
	P4:3464	16+56/335-	ACE	0.305 [0.11;0.50]	0.305 [0.11;0.50]	NS	0.508 [0.33;0.66]	0.187[0.13;0.27]
	P4:3374	16+56/335+337-158a-	ACE	0.475 [0.26;0.70]	0.475 [0.26;0.70]	NS	0.336 [0.12;0.51]	0.188[0.14;0.27]
	P4:2677	16+56/335+337-158a-R7-	ACE	0.472 [0.26;0.70]	0.472 [0.26;0.70]	NS	0.339 [0.13;0.51]	0.189 [0.14;0.27]
	P4:3455	16+56/335+337-	ACE	0.309 [0.12;0.50]	0.309 [0.12;0.50]	NS	0.505 [0.33;0.65]	0.186 [0.13;0.27]
	P4:2758	16+56/335+337-R7-	ACE	0.306 [0.11;0.50]	0.309 [0.12;0.50]	NS	0.506 [0.33;0.66]	0.187 [0.13;0.27]
	P4:3243	16+56/CD2+314+335+158b-	ACE	0.461 [0.23;0.71]	0.461 [0.23;0.71]	NS	0.322 [0.10;0.51]	0.217 [0.16;0.31]
	P4:2562	16+56/CD2+314+335+158b-R7-	ACE	0.465 [0.23;0.71]	0.465 [0.23;0.71]	NS	0.32 [0.09;0.51]	0.215 [0.15;0.30]
	P4:3162	16+56/CD2+314+335+158a-158b-	AE	0.788 [0.71;0.84]	0.788 [0.71;0.84]	NS	NS	0.212 [016;0.29]
	P4:2489	16+56/CD2+314+335+158a-158b-R7-	AE	0.79 [0.71;0.85]	0.79 [0.71;0.85]	NS	NS	0.21 [015;0.29]
	P4:3216	16+56/CD2+314+335+337-158b-	ACE	0.459 [0.22;0.70]	0.459 [0.22;0.70]	NS	0.323 [0.10;0.51]	0.218 [0.16;0.31]
	P4:2535	16+56/CD2+314+335+337-158b-R7-	ACE	0.46 [0.23;0.70]	0.46 [0.23;0.70]	NS	0.324 [0.10;0.51]	0.216 [0.16;0.31]
	P4:18	16+56/CD2+314+335+337-158a-158b-R7-	AE	0.788 [0.71;0.84]	0.788 [0.71;0.84]	NS	NS	0.212 [016;0.29]
	P4:2486	16+56/CD2+335+158a-158b-R7-	AE	0.782 [0.70;0.84]	0.782 [0.70;0.84]	NS	NS	0.218 [016;0.30]
	P4:2559	16+56/CD2+335+158b-R7-	ACE	0.471 [0.24;0.72]	0.471 [0.24;0.72]	NS	0.312 [0.08;0.50]	0.217 [0.16;0.31]
	P4:3159	16+56/CD2+335+158a-158b-	AE	0.78 [0.70;0.84]	0.78 [0.70;0.84]	NS	NS	0.22 [016;0.30]
	P4:3240	16+56/CD2+335+158b-	ACE	0.466 [0.23;0.71]	0.466 [0.23;0.71]	NS	0.314 [0.09;0.51]	0.219 [0.15;0.30]
	P4:3135	16+56/CD2+314+335+337-158a-158b-	AE	0.786 [0.71;0.84]	0.786 [0.71;0.84]	NS	NS	0.214 [016;0.29]
	P4:2532	16+56/CD2+335+337-158b-R7-	ACE	0.47 [0.24;0.72]	0.47 [0.24;0.72]	NS	0.313 [0.08;0.50]	0.217 [0.16;0.31]
	P4:3213	16+56/CD2+335+337-158b-	ACE	0.467 [0.23;0.71]	0.467 [0.23;0.71]	NS	0.314 [0.08;0.51]	0.22 [0.16;0.31]
	P4:3132	16+56/CD2+335+337-158a-158b-	AE	0.78 [0.70;0.84]	0.78 [0.70;0.84]	NS	NS	0.22 [0.16;0.30]
	P4:2461	16+56/CD2+335+337-158a-158b-R7-	AE	0.781 [0.70;0.84]	0.781 [0.70;0.84]	NS	NS	0.219 [0.16;0.30]
	P4:2967	16+56/335-337-158b+R7-	AE	0.772 [0.68;0.84]	0.772 [0.68;0.84]	NS	NS	0.228 [0.16;0.32]
	P4:2994	16+56/335-158b+R7-	AE	0.772 [0.68;0.84]	0.772 [0.68;0.84]	NS	NS	0.228 [0.16;0.32]
	P4:3707	16+56/335-158b+	AE	0.775 [0.68;0.84]	0.775 [0.68;0.84]	NS	NS	0.225 [0.16;0.32]
	P4:3680	16+56/335-337-158b+	AE	0.775 [0.68;0.84]	0.775 [0.68;0.84]	NS	NS	0.225 [0.16;0.32]
	P4:2970	16+56/314+335-337-158b+R7-	AE	0.775 [0.68;0.84]	0.775 [0.68;0.84]	NS	NS	0.225 [0.16;0.32]
	P4:3683	16+56/314+335-337-158b+	AE	0.776 [0.68;0.84]	0.776 [0.68;0.84]	NS	NS	0.224 [0.16;0.31]
	P4:2997	16+56/314+335-158b+R7-	AE	0.775 [0.68;0.84]	0.775 [0.68;0.84]	NS	NS	0.225 [0.16;0.32]
	P4:3710	16+56/314+335-158b+	AE	0.777 [0.69;0.84]	0.777 [0.69;0.84]	NS	NS	0.223 [0.16;0.31]
	P4:2900	16+56/335-337-158a-158b+R7-	AE	0.756 [0.66;0.82]	0.756 [0.66;0.82]	NS	NS	0.244 [018;0.34]

Table S9: Heritability of 1,113 proteins in the TwinsUK cohort
h2= heritability; CI_2.5=confidence interval at 2.5; CI_97.5=confidence interval at 97.5; A=additive genetic variance; D= dominance genetic variance; C= common environmental variance; E= unique environmental variance

SomaID	Target	UniProt	Entrez Gene ID	Entrez Gene Symbol	Units	SomaQC	Associated with AITD	Associated with one ot 17 AITD-IgG N-glycan structures	best model	h2 estimated	h2 CI_2.50	h2 CI_97.50	A estimation	A CI_2.50	A CI_97.50	D estimation	D CI_2.50	D CI_97.50	C estimation	C CI_2.50	C CI_97.50	E estimation	E CI_2.50	E CI_97.50
SL000125	IL-1a	P01583	3552	IL1A	RFU		Yes	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000589	TSH	P01215 P01	1081 1237	CGA TSHB	RFU		Yes	No	DE	0.356	0.229	0.402	0	0	0	0.356	0.122	0.591	0	0	0	0.644	0.409	0.878
SL003710	Caspase-2	P42575	835	CASP2	RFU		Yes	No	DE	0.470	0.443	0.479	0	0	0	0.470	0.238	0.701	0	0	0	0.530	0.299	0.762
SL000283	b2-Microglobulin	P61769	567	B2M	RFU		No	Yes	CE	0	0	0	0	0	0	0	0	0	0.509	0.356	0.662	0.491	0.338	0.644
SL002644	ERBB1	P00533	1956	EGFR	RFU		No	Yes	CE	0	0	0	0	0	0	0	0	0	0.389	0.208	0.569	0.611	0.431	0.792
SL008609	FCG3B	O75015	2215	FCGR3B	RFU		No	Yes	AE	0.479	0.468	0.485	0.479	0.303	0.655	0	0	0	0	0	0	0.521	0.345	0.697
SL000002	VEGF	P15692	7422	VEGFA	RFU		No	No	DE	0.500	0.499	0.500	0	0	0	0.500	0.302	0.697	0	0	0	0.500	0.303	0.698
SL000003	Angiogenin	P03950	283	ANG	RFU		No	No	AE	0.718	0.782	0.677	0.718	0.603	0.832	0	0	0	0	0	0	0.282	0.168	0.397
SL000004	bFGF	P09038	2247	FGF2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000006	PAI-1	P05121	5054	SERPINE1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.497	0.343	0.650	0.503	0.350	0.657
SL000007	ER	P03372	2099	ESR1	RFU		No	No	DE	0.742	0.827	0.692	0	0	0	0.742	0.613	0.872	0	0	0	0.258	0.128	0.387
SL000009	ERBB2	P04626	2064	ERBB2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000017	vWF	P04275	7450	VWF	RFU		No	No	AE	0.700	0.776	0.657	0.700	0.563	0.838	0	0	0	0	0	0	0.300	0.162	0.437
SL000019	Apo A-I	P02647	335	APOA1	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL000020	Apo B	P04114	338	APOB	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.617	0.491	0.744	0.383	0.256	0.509
SL000021	Insulin	P01308	3630	INS	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000022	D-dimer	P02671 P02	2243 2244	FGA FGB FGG	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.279	0.086	0.471	0.721	0.529	0.914
SL000024	TF	P13726	2152	F3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.383	0.208	0.558	0.617	0.442	0.792
SL000027	COX-2	P35354	5743	PTGS2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000038	MCP-1	P13500	6347	CCL2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.220	0.026	0.414	0.780	0.586	0.974
SL000039	IL-8	P10145	3576	IL8	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000045	IGFBP-3	P17936	3486	IGFBP3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.423	0.253	0.594	0.577	0.406	0.747
SL000047	IGF-I	P05019	3479	IGF1	RFU		No	No	DE	0.296	0.114	0.361	0	0	0	0.296	0.060	0.532	0	0	0	0.704	0.468	0.940
SL000048	Protein C	P04070	5624	PROC	RFU		No	No	AE	0.444	0.405	0.460	0.444	0.238	0.650	0	0	0	0	0	0	0.556	0.350	0.762
SL000049	Protein S	P07225	5627	PROS1	RFU		No	No	AE	0.296	0.145	0.357	0.296	0.083	0.509	0	0	0	0	0	0	0.704	0.491	0.917
SL000051	CRP	P02741	1401	CRP	RFU		No	No	AE	0.413	0.358	0.437	0.413	0.219	0.606	0	0	0	0	0	0	0.587	0.394	0.781
SL000053	tPA	P00750	5327	PLAT	RFU		No	No	AE	0.531	0.550	0.522	0.531	0.342	0.720	0	0	0	0	0	0	0.469	0.280	0.658
SL000055	Cadherin E	P12830	999	CDH1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.452	0.284	0.621	0.548	0.379	0.716
SL000057	Thymidine kise	P04183	7083	TK1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.275	0.079	0.471	0.725	0.529	0.921
SL000062	PSA	P07288	354	KLK3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000064	Kallikrein 7	P49862	5650	KLK7	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.573	0.435	0.711	0.427	0.289	0.565
SL000070	Glypican 3	P51654	2719	GPC3	RFU		No	No	DE	0	0	0	0	0	0	0.581	0.411	0.752	0	0	0	0.419	0.248	0.589
SL000076	p27Kip1	P46527	1027	CDKN1B	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000087	IL-6	P05231	3569	IL6	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.270	0.081	0.460	0.730	0.540	0.919
SL000088	TGF-b2	P61812	7042	TGFB2	RFU		No	No	DE	0.437	0.364	0.459	0	0	0	0.437	0.168	0.706	0	0	0	0.563	0.294	0.832
SL000089	TGF-b3	P10600	7043	TGFB3	RFU		No	No	DE	0.250	-0.083	0.341	0	0	0	0.250	-0.036	0.536	0	0	0	0.750	0.464	1.036
SL000091	PSA-ACT	P07288 P0	354 12	KLK3 SERPI3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.323	0.135	0.510	0.677	0.490	0.865
SL000104	Bcl-2	P10415	596	BCL2	RFU		No	No	AE	0.190	-0.116	0.293	0.190	-0.058	0.439	0	0	0	0	0	0	0.810	0.561	1.058
SL000124	MMP-2	P08253	4313	MMP2	RFU		No	No	AE	0.593	0.640	0.570	0.593	0.425	0.762	0	0	0	0	0	0	0.407	0.238	0.575
SL000130	Cyclin B1	P14635	891	CCNB1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000131	PC	P12004	5111	PC	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000133	MIP-3a	P78556	6364	CCL20	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000134	Met	P08581	4233	MET	RFU		No	No	AE	0.563	0.596	0.547	0.563	0.395	0.732	0	0	0	0	0	0	0.437	0.268	0.605
SL000136	AREG	P15514	374	AREG	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.713	0.612	0.813	0.287	0.187	0.388
SL000138	HB-EGF	Q99075	1839	HBEGF	RFU		No	No	AE	0.587	0.632	0.565	0.587	0.416	0.758	0	0	0	0	0	0	0.413	0.242	0.584
SL000139	EPI	O14944	2069	EREG	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000142	TS	P04818	7298	TYMS	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000158	PSMA	Q04609	2346	FOLH1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000164	Myoglobin	P02144	4151	MB	RFU		No	No	AE	0.542	0.564	0.531	0.542	0.370	0.714	0	0	0	0	0	0	0.458	0.286	0.630
SL000247	6-Phosphoglucote deh	P52209	5226	PGD	RFU		No	No	AE	0.817	0.878	0.773	0.817	0.737	0.898	0	0	0	0	0	0	0.183	0.102	0.263
SL000248	a1-Antichymotrypsin	P01011	12	SERPI3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.278	0.083	0.473	0.722	0.527	0.917
SL000249	a1-Antitrypsin	P01009	5265	SERPI1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.346	0.165	0.527	0.654	0.473	0.835
SL000250	a2-Antiplasmin	P08697	5345	SERPINF2	RFU		No	No	DE	0.679	0.795	0.628	0	0	0	0.679	0.482	0.876	0	0	0	0.321	0.124	0.518
SL000251	a2-HS-Glycoprotein	P02765	197	AHSG	RFU		No	No	AE	0.442	0.401	0.459	0.442	0.235	0.649	0	0	0	0	0	0	0.558	0.351	0.765
SL000252	a2-Macroglobulin	P01023	2	A2M	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.602	0.471	0.733	0.398	0.267	0.529
SL000254	Albumin	P02768	213	ALB	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.562	0.419	0.704	0.438	0.296	0.581
SL000268	Angiostatin	P00747	5340	PLG	RFU		No	No	AE	0.733	0.795	0.693	0.733	0.628	0.838	0	0	0	0	0	0	0.267	0.162	0.372
SL000271	Angiotensinogen	P01019	183	AGT	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.395	0.220	0.571	0.605	0.429	0.780
SL000272	Antithrombin III	P01008	462	SERPINC1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.350	0.149	0.552	0.650	0.448	0.851
SL000276	Apo E	P02649	348	APOE	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL000277	Apo E2	P02649	348	APOE	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.675	0.564	0.787	0.325	0.213	0.436
SL000280	GOT1	P17174	2805	GOT1	RFU		No	No	DE	0	0	0	0	0	0	0.588	0.412	0.763	0	0	0	0.412	0.237	0.588
SL000299	b-ECGF	P05230	2246	FGF1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000300	b-Endorphin	P01189	5443	POMC	RFU		No	No	AE	0.524	0.537	0.518	0.524	0.354	0.694	0	0	0	0	0	0	0.476	0.306	0.646
SL000305	b-NGF	P01138	4803	NGF	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000306	BNP-32	P16860	4879	NPPB	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000308	C1-Esterase Inhibitor	P05155	710	SERPING1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.621	0.494	0.747	0.379	0.253	0.506
SL000309	C1q	P02745 P0	712 713 71	C1QA C1QB C1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000310	C1r	P00736	715	C1R	RFU		No	No	AE	0.440	0.400	0.457	0.440	0.240	0.640	0	0	0	0	0	0	0.560	0.360	0.760
SL000311	C1s	P09871	716	C1S	RFU		No	No	AE	0.423	0.368	0.446	0.423	0.214	0.633	0	0	0	0	0	0	0.577	0.367	0.786
SL000312	C3	P01024	718	C3	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL000313	C3a	P01024	718	C3	RFU		No	No	DE	0.631	0.697	0.598	0	0	0	0.631	0.463	0.798	0	0	0	0.369	0.202	0.537
SL000314	C3b	P01024	718	C3	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL000316	C4	P0C0L4 P0	720 721	C4A C4B	RFU		No	No	DE	0.748	0.816	0.704	0	0	0	0.748	0.641	0.855	0	0	0	0.252	0.145	0.359
SL000318	C4b	P0C0L4 P0	720 721	C4A C4B	RFU		No	No	DCE	0.256	0.005	0.320	0	0	0	0.256	0.002	0.509	0.522	0.284	0.761	0.222	0.123	0.321
SL000319	C5	P01031	727	C5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.390	0.209	0.570	0.610	0.430	0.791
SL000320	C5a	P01031	727	C5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.529	0.383	0.676	0.471	0.324	0.617
SL000321	C5b 6 Complex	P01031 P13	727 729	C5 C6	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.434	0.263	0.605	0.566	0.395	0.737
SL000322	C6	P13671	729	C6	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.308	0.122	0.495	0.692	0.505	0.878
SL000323	C7	P10643	730	C7	RFU		No	No	AE	0.448	0.410	0.463	0.448	0.240	0.655	0	0	0	0	0	0	0.552	0.345	0.760
SL000324	C8	P07357 P07	731 732 73	C8A C8B C8G	RFU		No	No	DE	0.535	0.560	0.525	0	0	0	0.535	0.330	0.741	0	0	0	0.465	0.259	0.670
SL000325	C9	P02748	735	C9	RFU		No	No	AE	0.502	0.503	0.501	0.502	0.306	0.698	0	0	0	0	0	0	0.498	0.302	0.694
SL000337	Calpain I	P07384 P04	823 826	CAPN1 CAPNS1	RFU		No	No	AE	0.727	0.792	0.686	0.727	0.616	0.838	0	0	0	0	0	0	0.273	0.162	0.384
SL000338	Calpastatin	P20810	831	CAST	RFU		No	No	AE	0.581	0.617	0.562	0.581	0.427	0.736	0	0	0	0	0	0	0.419	0.264	0.573
SL000339	carbonic anhydrase II	P00918	760	CA2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000342	Catalase	P04040	847	CAT	RFU		No	No	AE	0.487	0.477	0.490	0.487	0.285	0.688	0	0	0	0	0	0	0.513	0.312	0.715

SL000343	Cathepsin B	P07858	1508	CTSB	RFU		No	No	AE	0.494	0.491	0.496	0.494	0.321	0.668	0	0	0	0	0	0	0.506	0.332	0.679
SL000344	Cathepsin D	P07339	1509	CTSD	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000345	Cathepsin G	P08311	1511	CTSG	RFU		No	No	DE	0.415	0.139	0.452	0	0	0	0.415	0.033	0.797	0	0	0	0.585	0.203	0.967
SL000346	Cathepsin H	P09668	1512	CTSH	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.557	0.414	0.701	0.443	0.299	0.586
SL000347	CBG	P08185	866	SERPI6	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000357	Coagulation Factor IX	P00740	2158	F9	RFU		No	No	AE	0.515	0.524	0.511	0.515	0.327	0.704	0	0	0	0	0	0	0.485	0.296	0.673
SL000358	Coagulation Factor VII	P08709	2155	F7	RFU		No	No	DE	0.730	0.803	0.686	0	0	0	0.730	0.610	0.850	0	0	0	0.270	0.150	0.390
SL000360	Coagulation Factor X	P00742	2159	F10	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.396	0.218	0.573	0.604	0.427	0.782
SL000377	CK-BB	P12277	1152	CKB	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000382	CK-MB	P12277	P06 1152	1158	CKB CKM	RFU	No	No	AE	0.550	0.577	0.537	0.550	0.376	0.725	0	0	0	0	0	0	0.450	0.275	0.624
SL000383	CK-MM	P06732	1158	CKM	RFU		No	No	AE	0.546	0.573	0.534	0.546	0.364	0.728	0	0	0	0	0	0	0.454	0.272	0.636
SL000384	CTLA-4	P16410	1493	CTLA4	RFU		No	No	DE	0.463	0.377	0.478	0	0	0	0.463	0.114	0.812	0	0	0	0.537	0.188	0.886
SL000396	Cytochrome c	P99999	54205	CYCS	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000398	Cytochrome P450 3A4	P08684	1576	CYP3A4	RFU		No	No	AE	0.721	0.789	0.679	0.721	0.604	0.839	0	0	0	0	0	0	0.279	0.161	0.396
SL000401	Elastase	P08246	1991	ELANE	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000403	Endostatin	P39060	80781	COL18A1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.687	0.578	0.797	0.313	0.203	0.422
SL000406	Eotaxin	P51671	6356	CCL11	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.275	0.085	0.465	0.725	0.535	0.915
SL000408	Epo	P01588	2056	EPO	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000409	ERK-1	P27361	5595	MAPK3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.513	0.363	0.663	0.487	0.337	0.637
SL000414	Factor B	P00751	629	CFB	RFU		No	No	DE	0.405	0.325	0.435	0	0	0	0.405	0.177	0.633	0	0	0	0.595	0.367	0.823
SL000415	Factor H	P08603	3075	CFH	RFU		No	No	DE	0.371	0.252	0.413	0	0	0	0.371	0.131	0.612	0	0	0	0.629	0.388	0.869
SL000420	Ferritin	P02794	P02 2495	2512	FTH1 FTL	RFU	No	No	AE	0.623	0.673	0.595	0.623	0.479	0.768	0	0	0	0	0	0	0.377	0.232	0.521
SL000424	Fibrinogen	P02671	P02 2243	2244	FGA FGB FGG	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.226	0.024	0.428	0.774	0.572	0.976
SL000426	Fibronectin	P02751	2335	FN1	RFU		No	No	AE	0.627	0.683	0.598	0.627	0.476	0.779	0	0	0	0	0	0	0.373	0.221	0.524
SL000427	Fractalkine/CX3CL-1	P78423	6376	CX3CL1	RFU		No	No	AE	0.405	0.349	0.430	0.405	0.220	0.589	0	0	0	0	0	0	0.595	0.411	0.780
SL000428	FSH	P01215	P0 1081	2488	CGA FSHB	RFU	No	No	DE	0.298	0.157	0.357	0	0	0	0.298	0.157	0.357	0	0	0	0.702	0.497	0.908
SL000433	Glucagon	P01275	2641	GCG	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.539	0.394	0.683	0.461	0.317	0.606
SL000437	Haptoglobin Mixed Ty	P00738	3240	HP	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.370	0.195	0.546	0.630	0.454	0.805
SL000440	Hemopexin	P02790	3263	HPX	RFU		No	No	AE	0.905	0.944	0.872	0.905	0.860	0.949	0	0	0	0	0	0	0.095	0.051	0.140
SL000441	HGF	P14210	3082	HGF	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000445	HIV-2 Rev	P18093	1724716	Human-virus	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000449	HSP 40	P25685	3337	DJB1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.211	0.013	0.408	0.789	0.592	0.987
SL000450	HSP 60	P10809	3329	HSPD1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.546	0.403	0.689	0.454	0.311	0.597
SL000451	HSP 70	P08107	3303	HSPA1A	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.345	0.163	0.527	0.655	0.473	0.837
SL000456	iC3b	P01024	718	C3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.496	0.339	0.653	0.504	0.347	0.661
SL000458	IFN-g R1	P15260	3459	IFNGR1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000460	IgD	P01880	3495	50802	IGHD IGK@ IGL(	RFU	No	No	DE	0.454	0.423	0.467	0	0	0	0.454	0.256	0.652	0	0	0	0.546	0.348	0.744
SL000461	IgE	P01854	3497	5080	IGHE IGK@ IGL@	RFU	No	No	AE	0.557	0.586	0.542	0.557	0.384	0.729	0	0	0	0	0	0	0.443	0.271	0.616
SL000462	IGFBP-1	P08833	3484	IGFBP1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.567	0.429	0.705	0.433	0.295	0.571
SL000466	IGFBP-2	P18065	3485	IGFBP2	RFU		No	No	AE	0.527	0.541	0.520	0.527	0.352	0.701	0	0	0	0	0	0	0.473	0.299	0.648
SL000467	IgG	P01857	3500	3501	IGHG1 IGHG2 IG	RFU	No	No	DE	0.502	0.503	0.501	0	0	0	0.502	0.316	0.688	0	0	0	0.498	0.312	0.684
SL000468	IgM	P01871	3507	3512	IGHM IGJ IGK@ I	RFU	No	No	AE	0.432	0.392	0.451	0.432	0.247	0.617	0	0	0	0	0	0	0.568	0.383	0.753
SL000470	IL-11	P20809	3589	IL11	RFU		No	No	DE	0.344	0.196	0.395	0	0	0	0.344	0.101	0.587	0	0	0	0.656	0.413	0.899
SL000474	IL-16	Q14005	3603	IL16	RFU		No	No	AE	0.658	0.723	0.622	0.658	0.512	0.804	0	0	0	0	0	0	0.342	0.196	0.488
SL000478	IL-2	P60568	3558	IL2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.584	0.449	0.719	0.416	0.281	0.551
SL000479	IL-3	P08700	3562	IL3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000480	IL-4	P05112	3565	IL4	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000481	IL-5	P05113	3567	IL5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.416	0.245	0.587	0.584	0.413	0.755
SL000483	IL-7	P13232	3574	IL7	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000493	LDH-H 1	P07195	3945	LDHB	RFU		No	No	AE	0.709	0.772	0.669	0.709	0.593	0.824	0	0	0	0	0	0	0.291	0.176	0.407
SL000496	Lactoferrin	P02788	4057	LTF	RFU		No	No	DE	0.605	0.650	0.581	0	0	0	0.605	0.455	0.755	0	0	0	0.395	0.245	0.545
SL000497	Laminin	P25391	P0 284217	391	LAMA1 LAMB1 I	RFU	No	No	AE	0.616	0.668	0.589	0.616	0.461	0.771	0	0	0	0	0	0	0.384	0.229	0.539
SL000498	Leptin	P41159	3952	LEP	RFU		No	No	AE	0.622	0.680	0.593	0.622	0.462	0.783	0	0	0	0	0	0	0.378	0.217	0.538
SL000506	Luteinizing hormone	P01215	P0 1081	3972	CGA LHB	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.305	0.119	0.490	0.695	0.510	0.881
SL000507	Lymphotoxin a1/b2	P01374	Q0 4049	4050	LTA LTB	RFU	No	No	DE	0.538	0.568	0.526	0	0	0	0.538	0.317	0.759	0	0	0	0.462	0.241	0.683
SL000508	Lymphotoxin a2/b1	P01374	Q0 4049	4050	LTA LTB	RFU	No	No	CE	0	0	0	0	0	0	0	0	0	0.296	0.103	0.489	0.704	0.511	0.897
SL000509	Lymphotoxin b R	P36941	4055	LTBR	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.274	0.080	0.468	0.726	0.532	0.920
SL000510	Lysozyme	P61626	4069	LYZ	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.682	0.570	0.795	0.318	0.205	0.430
SL000515	MCP-2	P80075	6355	CCL8	RFU		No	No	DE	0.388	0.300	0.422	0	0	0	0.388	0.168	0.608	0	0	0	0.612	0.392	0.832
SL000516	MCP-3	P80098	6354	CCL7	RFU		No	No	DE	0.760	0.833	0.713	0	0	0	0.760	0.650	0.870	0	0	0	0.240	0.130	0.350
SL000517	MCP-4	Q99616	6357	CCL13	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.172	-0.027	0.372	0.828	0.628	1.027
SL000519	MIP-1a	P10147	6348	CCL3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.154	-0.045	0.354	0.846	0.646	1.045
SL000521	MMP-1	P03956	4312	MMP1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.367	0.191	0.543	0.633	0.457	0.809
SL000522	MMP-12	P39900	4321	MMP12	RFU		No	No	AE	0.595	0.639	0.572	0.595	0.435	0.755	0	0	0	0	0	0	0.405	0.245	0.565
SL000523	MMP-13	P45452	4322	MMP13	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000524	MMP-3	P08254	4314	MMP3	RFU		No	No	AE	0.203	-0.032	0.294	0.203	-0.018	0.424	0	0	0	0	0	0	0.797	0.576	1.018
SL000525	MMP-7	P09237	4316	MMP7	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.570	0.431	0.708	0.430	0.292	0.569
SL000526	MMP-8	P22894	4317	MMP8	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.477	0.319	0.636	0.523	0.364	0.681
SL000527	MMP-9	P14780	4318	MMP9	RFU		No	No	DE	0.780	0.845	0.736	0	0	0	0.780	0.686	0.874	0	0	0	0.220	0.126	0.314
SL000528	DPH-P450 Oxidoredu	P16435	5447	POR	RFU		No	No	AE	0.332	0.207	0.382	0.332	0.118	0.545	0	0	0	0	0	0	0.668	0.455	0.882
SL000530	OSM	P13725	5008	OSM	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.278	0.085	0.472	0.722	0.528	0.915
SL000532	ON	P09486	6678	SPARC	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.409	0.240	0.579	0.591	0.421	0.760
SL000535	PDGF-AA	P04085	5154	PDGFA	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.397	0.226	0.569	0.603	0.431	0.774
SL000537	PDGF-BB	P01127	5155	PDGFB	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.460	0.300	0.621	0.540	0.379	0.700
SL000539	PHI	P06744	2821	GPI	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.502	0.349	0.655	0.498	0.345	0.651
SL000540	Plasmin	P00747	5340	PLG	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000541	Plasminogen	P00747	5340	PLG	RFU		No	No	DE	0.591	0.640	0.568	0	0	0	0.591	0.417	0.766	0	0	0	0.409	0.234	0.583
SL000542	gpIIbIIIa	P08514	P05 3674	3690	ITGA2B ITGB3	RFU	No	No	AE	0.695	0.762	0.655	0.695	0.566	0.824	0	0	0	0	0	0	0.305	0.176	0.434
SL000545	Prekallikrein	P03952	3818	KLKB1	RFU		No	No	AE	0.544	0.569	0.532	0.544	0.362	0.726	0	0	0	0	0	0	0.456	0.274	0.638
SL000546	PRL	P01236	5617	PRL	RFU		No	No	DE	0.541	0.578	0.528	0	0	0	0.541	0.304	0.778	0	0	0	0.459	0.222	0.696
SL000550	PCI	P05154	5104	SERPI5	RFU		No	No	AE	0.689	0.750	0.651	0.689	0.566	0.811	0	0	0	0	0	0	0.311	0.189	0.434
SL000551	PKC-A	P17252	5578	PRKCA	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.562	0.423	0.702	0.438	0.298	0.577
SL000553	PKC-B-II	P05771	5579	PRKCB	RFU		No	No	AE	0.745	0.810	0.703	0.745	0.641	0.849	0	0	0	0	0	0	0.255	0.151	0.359
SL000554	PKC-D	Q05655	5580	PRKCD	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000556	PKC-G	P05129	5582	PRKCG	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000557	PKC-Z	Q05513	5590	PRKCZ	RFU		No	No	DE	0.271	0.059	0.345	0	0	0	0.271	0.031	0.511	0	0	0	0.729	0.489	0.969
SL000558	Prothrombin	P00734	2147	F2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.181	-0.025	0.388	0.819	0.612	1.025
SL000560	P-Selectin	P16109	6403	SELP	RFU		No	No	AE	0.732	0.798	0.690	0.732	0.622	0.843	0	0	0	0	0	0	0.268	0.157	0.378
SL000563	RANTES	P13501	6352	CCL5	RFU		No	No	AE	0.487	0.478	0.490	0.487	0.292	0.682	0	0	0	0	0	0	0.513	0.318	0.708
SL000565	Renin	P00797	5972	REN	RFU		No	No	DE	0.467	0.445	0.477	0	0	0	0.467	0.265	0.670	0	0	0	0.533	0.330	0.735
SL000566	RBP	P02753	5950	RBP4	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000570	Secretin	P09683	6343	SCT	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000572	SAA	P0DJI8	6288	SAA1	RFU		No	No	AE	0.903	0.943	0.871	0.903	0.859	0.948	0	0	0	0	0	0	0.097	0.052	0.141

SL000573	SAP	P02743	325	APCS	RFU			No	No	AE	0.475	0.459	0.482	0.475	0.284	0.666	0	0	0	0	0	0	0.525	0.334	0.716
SL000581	SOD	P00441	6647	SOD1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.249	0.056	0.441	0.751	0.559	0.944
SL000582	Survivin	O15392	332	BIRC5	RFU			No	No	DE	0.759	0.852	0.705	0	0	0	0.759	0.627	0.891	0	0	0	0.241	0.109	0.373
SL000584	TGF-b1	P01137	7040	TGFB1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.227	0.032	0.423	0.773	0.577	0.968
SL000586	Thrombin	P00734	2147	F2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.596	0.465	0.728	0.404	0.272	0.535
SL000587	Thyroglobulin	P01266	7038	TG	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000588	TMA	P07202	7173	TPO	RFU			No	No	DE	0.513	0.537	0.508	0	0	0	0.513	0.180	0.845	0	0	0	0.487	0.155	0.820
SL000590	Thyroxine-Binding Glo	P05543	6906	SERPI7	RFU			No	No	DE	0.556	0.585	0.542	0	0	0	0.556	0.388	0.725	0	0	0	0.444	0.275	0.612
SL000591	TIMP-1	P01033	7076	TIMP1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.261	0.065	0.457	0.739	0.543	0.935
SL000592	TIMP-2	P16035	7077	TIMP2	RFU			No	No	AE	0.472	0.453	0.480	0.472	0.273	0.671	0	0	0	0	0	0	0.528	0.329	0.727
SL000597	TNF-b	P01374	4049	LTA	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000601	Transferrin	P02787	7018	TF	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.260	0.062	0.457	0.740	0.543	0.938
SL000603	Trypsin	P07477	5644	PRSS1	RFU			No	No	AE	0.600	0.649	0.575	0.600	0.434	0.765	0	0	0	0	0	0	0.400	0.235	0.566
SL000605	Ubiquitin+1	P62979	6233	RPS27A	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.449	0.284	0.614	0.551	0.386	0.716
SL000613	uPA	P00749	5328	PLAU	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.478	0.319	0.637	0.522	0.363	0.681
SL000615	Vasoactive Intestil Pep	P01282	7432	VIP	RFU			No	No	DE	0.546	0.575	0.533	0	0	0	0.546	0.349	0.743	0	0	0	0.454	0.257	0.651
SL000617	ALT	P24298	2875	GPT	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.340	0.158	0.522	0.660	0.478	0.842
SL000622	Coagulation Factor V	P12259	2153	F5	RFU			No	No	AE	0.701	0.764	0.662	0.701	0.581	0.821	0	0	0	0	0	0	0.299	0.179	0.419
SL000633	Fas ligand soluble	P48023	356	FASLG	RFU			No	No	DE	0.394	0.320	0.425	0	0	0	0.394	0.189	0.599	0	0	0	0.606	0.401	0.811
SL000638	Cadherin-2	P19022	1000	CDH2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000640	Nidogen	P14543	4811	NID1	RFU			No	No	AE	0.678	0.755	0.637	0.678	0.528	0.828	0	0	0	0	0	0	0.322	0.172	0.472
SL000645	MMP-10	P09238	4319	MMP10	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000655	Keratin 18	P05783	3875	KRT18	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000658	GAS1	P54826	2619	GAS1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000668	CD36 ANTIGEN	P16671	948	CD36	RFU			No	No	DE	0.584	0.629	0.562	0	0	0	0.584	0.408	0.759	0	0	0	0.416	0.241	0.592
SL000670	GSTA3	Q16772	2940	GSTA3	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL000674	FST	P19883	10468	FST	RFU			No	No	AE	0.213	-0.141	0.315	0.213	-0.063	0.488	0	0	0	0	0	0	0.787	0.512	1.063
SL000678	Granulysin	P22749	10578	GNLY	RFU			No	No	AE	0.679	0.740	0.643	0.679	0.552	0.806	0	0	0	0	0	0	0.321	0.194	0.448
SL000695	Lipocalin 2	P80188	3934	LCN2	RFU	Calibration Scale		No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL000836	Hemoglobin	P69905	P6	3039	3043	HBA1 HBB	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.397	0.225	0.569	0.603	0.431	0.775
SL001691	FGF7	P21781	2252	FGF7	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.602	0.470	0.733	0.398	0.267	0.530
SL001713	IL-17	Q16552	3605	IL17A	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.241	0.044	0.437	0.759	0.563	0.956
SL001716	IL-12	P29459	P2	3592	3593	IL12A IL12B	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001717	IL-10	P22301	3586	IL10	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001718	IL-13	P35225	3596	IL13	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001720	VCAM-1	P19320	7412	VCAM1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.388	0.212	0.564	0.612	0.436	0.788
SL001721	PECAM-1	P16284	5175	PECAM1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001726	GM-CSF	P04141	1437	CSF2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001729	G-CSF	P09919	1440	CSF3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.223	0.029	0.416	0.777	0.584	0.971
SL001737	STRATIFIN	P31947	2810	SFN	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.475	0.317	0.634	0.525	0.366	0.683
SL001753	Sialoadhesin	Q9BZZ2	6614	SIGLEC1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001766	HCG	P01215	P01	1081	1082	CGA CGB	RFU			No	No	DE	0.502	0.504	0.502	0	0	0	0.502	0.311	0.694	0	0	0	0.498	0.306	0.689
SL001774	FABP	P05413	2170	FABP3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.422	0.253	0.591	0.578	0.409	0.747
SL001777	Cystatin C	P01034	1471	CST3	RFU			No	No	DE	0.593	0.635	0.571	0	0	0	0.593	0.439	0.747	0	0	0	0.407	0.253	0.561
SL001795	IL-1b	P01584	3553	IL1B	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.169	-0.029	0.367	0.831	0.633	1.029
SL001796	Myeloperoxidase	P05164	4353	MPO	RFU			No	No	AE	0.600	0.644	0.576	0.600	0.447	0.753	0	0	0	0	0	0	0.400	0.247	0.553
SL001797	Kallikrein 6	Q92876	5653	KLK6	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.202	0.002	0.402	0.798	0.598	0.998
SL001800	TNF sR-II	P20333	7133	TNFRSF1B	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.493	0.337	0.650	0.507	0.350	0.663
SL001802	IFN-g	P01579	3458	IFNG	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.697	0.592	0.802	0.303	0.198	0.408
SL001815	Mn SOD	P04179	6648	SOD2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.488	0.330	0.646	0.512	0.354	0.670
SL001868	CASA	P47710	1446	CSN1S1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001888	SLPI	P03973	6590	SLPI	RFU			No	No	AE	0.529	0.543	0.521	0.529	0.362	0.695	0	0	0	0	0	0	0.471	0.305	0.638
SL001890	GA733-1 protein	P09758	4070	TACSTD2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001896	Clusterin	P10909	1191	CLU	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.363	0.184	0.542	0.637	0.458	0.816
SL001897	SPINT2	O43291	10653	SPINT2	RFU			No	No	AE	0.685	0.751	0.646	0.685	0.553	0.816	0	0	0	0	0	0	0.315	0.184	0.447
SL001902	BCAM	P50895	4059	BCAM	RFU			No	No	AE	0.523	0.543	0.516	0.523	0.290	0.757	0	0	0	0	0	0	0.477	0.243	0.710
SL001905	Mesothelin	Q13421	10232	MSLN	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001938	Activin A	P08476	3624	INHBA	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.318	0.134	0.501	0.682	0.499	0.866
SL001943	IL-6 sRa	P08887	3570	IL6R	RFU			No	No	AE	0.845	0.899	0.804	0.845	0.777	0.913	0	0	0	0	0	0	0.155	0.087	0.223
SL001945	sE-Selectin	P16581	6401	SELE	RFU			No	No	AE	0.723	0.792	0.680	0.723	0.605	0.841	0	0	0	0	0	0	0.277	0.159	0.395
SL001947	MIA	Q16674	8190	MIA	RFU			No	No	DE	0.669	0.730	0.634	0	0	0	0.669	0.538	0.801	0	0	0	0.331	0.199	0.462
SL001973	Mammaglobin 2	O75556	4246	SCGB2A1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL001992	TNF sR-I	P19438	7132	TNFRSF1A	RFU			No	No	AE	0.502	0.504	0.502	0.502	0.313	0.692	0	0	0	0	0	0	0.498	0.308	0.687
SL001995	Angiopoietin-1	Q15389	284	ANGPT1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.293	0.107	0.480	0.707	0.520	0.893
SL001996	Angiopoietin-2	O15123	285	ANGPT2	RFU			No	No	AE	0.666	0.726	0.632	0.666	0.535	0.798	0	0	0	0	0	0	0.334	0.202	0.465
SL001997	IL-1 sRI	P14778	3554	IL1R1	RFU			No	No	AE	0.539	0.560	0.529	0.539	0.362	0.715	0	0	0	0	0	0	0.461	0.285	0.638
SL001998	TFPI	P10646	7035	TFPI	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.540	0.392	0.687	0.460	0.313	0.608
SL001999	MDM2	Q00987	4193	MDM2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.220	0.026	0.415	0.780	0.585	0.974
SL002036	FGFR4	P22455	2264	FGFR4	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL002075	IFN-aA	P01563	3440	IF2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.836	0.774	0.898	0.164	0.102	0.226
SL002077	Alkaline phosphatase	P05186	249	ALPL	RFU			No	No	AE	0.592	0.635	0.570	0.592	0.435	0.749	0	0	0	0	0	0	0.408	0.251	0.565
SL002078	TGF-b R II	P37173	7048	TGFBR2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.149	-0.050	0.348	0.851	0.652	1.050
SL002081	Cadherin-5	P33151	1003	CDH5	RFU			No	No	DE	0.645	0.706	0.611	0	0	0	0.645	0.495	0.794	0	0	0	0.355	0.206	0.505
SL002086	Ficolin-3	O75636	8547	FCN3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.655	0.538	0.772	0.345	0.228	0.462
SL002093	Histone H2A.z	P0C0S5	3015	H2AFZ	RFU			No	No	DE	0.695	0.781	0.649	0	0	0	0.695	0.542	0.848	0	0	0	0.305	0.152	0.458
SL002506	suPAR	Q03405	5329	PLAUR	RFU			No	No	AE	0.538	0.560	0.528	0.538	0.357	0.719	0	0	0	0	0	0	0.462	0.281	0.643
SL002508	IL-18 BPa	O95998	10068	IL18BP	RFU			No	No	DE	0.296	0.135	0.358	0	0	0	0.296	0.075	0.516	0	0	0	0.704	0.484	0.925
SL002517	TNF-a	P01375	7124	TNF	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL002519	ERBB3	P21860	2065	ERBB3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.612	0.482	0.742	0.388	0.258	0.518
SL002522	Rb	P06400	5925	RB1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL002524	sCD4	P01730	920	CD4	RFU			No	No	DE	0.844	0.908	0.798	0	0	0	0.844	0.766	0.923	0	0	0	0.156	0.077	0.234
SL002525	C2	P06681	717	C2	RFU			No	No	AE	0.508	0.513	0.506	0.508	0.312	0.704	0	0	0	0	0	0	0.492	0.296	0.688
SL002528	NPS-PLA2	P14555	5320	PLA2G2A	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.650	0.531	0.768	0.350	0.232	0.469
SL002539	OPG	O00300	4982	TNFRSF11B	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.356	0.176	0.537	0.644	0.463	0.824
SL002541	sRANKL	O14788	8600	TNFSF11	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.269	0.075	0.462	0.731	0.538	0.925
SL002542	K-ras	P01116	3845	KRAS	RFU			No	No	DE	0.652	0.718	0.617	0	0	0	0.652	0.501	0.803	0	0	0	0.348	0.197	0.499
SL002561	PTHrP	P12272	5744	PTHLH	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.327	0.144	0.510	0.673	0.490	0.856
SL002621	Midkine	P21741	4192	MDK	RFU	Calibration Scale		No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL002640	PIGF	P49763	5228	PGF	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL002646	MMP-14	P50281	4323	MMP14	RFU			No	No	DE	0.372	0.077	0.425	0	0	0	0.372	0.023	0.721	0	0	0	0.628	0.279	0.977
SL002650	M2-PK	P14618	5315	PKM2	RFU			No	No	AE	0.731	0.798	0.689	0.731	0.620	0.843	0	0	0	0	0	0	0.269	0.157	0.380
SL002654	Epithelial cell kise	P29317	1969	EPHA2	RFU			No	No	DE	0.443	0.404	0.460	0	0	0	0.443	0.239	0.648	0	0	0	0.557	0.352	0.761
SL002655	CTGF	P29279	1490	CTGF	RFU			No	No	AE	0.509	0.514	0.506	0.509	0.319	0.699	0	0	0	0	0	0	0.491	0.301	0.681

SL002662	Coagulation Factor XI	P03951	2160	F11	RFU			No	No	AE	0.514	0.523	0.511	0.514	0.334	0.695	0	0	0	0	0	0	0.486	0.305	0.666
SL002684	CSF-1	P09603	1435	CSF1	RFU			No	No	DE	0.434	0.335	0.459	0	0	0	0.434	0.133	0.736	0	0	0	0.566	0.264	0.867
SL002695	Glutamate carboxypep	Q96KP4	55748	CNDP2	RFU			No	No	DE	0.534	0.566	0.523	0	0	0	0.534	0.291	0.777	0	0	0	0.466	0.223	0.709
SL002702	PIM1	P11309	5292	PIM1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL002704	PTN	P21246	5764	PTN	RFU			No	No	DE	0.336	0.185	0.389	0	0	0	0.336	0.096	0.576	0	0	0	0.664	0.424	0.904
SL002705	Thrombospondin-1	P07996	7057	THBS1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.369	0.193	0.545	0.631	0.455	0.807
SL002706	CD23	P06734	2208	FCER2	RFU			No	No	AE	0.521	0.533	0.516	0.521	0.346	0.696	0	0	0	0	0	0	0.479	0.304	0.654
SL002755	PAPP-A	Q13219	5069	PAPPA	RFU			No	No	DE	0.724	0.792	0.681	0	0	0	0.724	0.607	0.841	0	0	0	0.276	0.159	0.393
SL002756	hnRNP K	P61978	3190	HNRNPK	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL002763	Kallikrein 11	Q9UBX7	11012	KLK11	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.595	0.462	0.728	0.405	0.272	0.538
SL002783	Cardiotrophin-1	Q16619	1489	CTF1	RFU			No	No	DE	0.366	0.194	0.414	0	0	0	0.366	0.085	0.647	0	0	0	0.634	0.353	0.915
SL002792	BARK1	P25098	156	ADRBK1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.595	0.463	0.727	0.405	0.273	0.537
SL002803	PGP9.5	P09936	7345	UCHL1	RFU			No	No	AE	0.742	0.818	0.695	0.742	0.623	0.861	0	0	0	0	0	0	0.258	0.139	0.377
SL002823	sL-Selectin	P14151	6402	SELL	RFU			No	No	DE	0.301	0.136	0.363	0	0	0	0.301	0.074	0.528	0	0	0	0.699	0.472	0.926
SL002922	sICAM-1	P05362	3383	ICAM1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.573	0.435	0.710	0.427	0.290	0.565
SL003041	PF-4	P02776	5196	PF4	RFU	Calibration Scale		No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL003043	TIMP-3	P35625	7078	TIMP3	RFU			No	No	AE	0.569	0.603	0.552	0.569	0.407	0.732	0	0	0	0	0	0	0.431	0.268	0.593
SL003060	bFGF-R	P11362	2260	FGFR1	RFU			No	No	DE	0.524	0.538	0.518	0	0	0	0.524	0.342	0.707	0	0	0	0.476	0.293	0.658
SL003080	MIF	P14174	4282	MIF	RFU			No	No	AE	0.621	0.678	0.591	0.621	0.460	0.782	0	0	0	0	0	0	0.379	0.218	0.540
SL003104	Eotaxin-2	O00175	6369	CCL24	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003166	ALCAM	Q13740	214	ALCAM	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.446	0.274	0.618	0.554	0.382	0.726
SL003167	BLC	O43927	10563	CXCL13	RFU			No	No	AE	0.380	0.291	0.416	0.380	0.166	0.595	0	0	0	0	0	0	0.620	0.405	0.834
SL003168	CTACK	Q9Y4X3	10850	CCL27	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.170	-0.035	0.376	0.830	0.624	1.035
SL003169	E-78	P42830	6374	CXCL5	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.266	0.071	0.461	0.734	0.539	0.929
SL003171	FGF-4	P08620	2249	FGF4	RFU			No	No	DE	0.540	0.579	0.527	0	0	0	0.540	0.295	0.785	0	0	0	0.460	0.215	0.705
SL003172	GCP-2	P80162	6372	CXCL6	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.417	0.249	0.586	0.583	0.414	0.751
SL003173	Gro-a	P09341	2919	CXCL1	RFU			No	No	AE	0.568	0.606	0.550	0.568	0.388	0.748	0	0	0	0	0	0	0.432	0.252	0.612
SL003176	I-309	P22362	6346	CCL1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.279	0.087	0.472	0.721	0.528	0.913
SL003177	sICAM-2	P13598	3384	ICAM2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.162	-0.045	0.368	0.838	0.632	1.045
SL003178	sICAM-3	P32942	3385	ICAM3	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003179	Integrin a1b1	P56199	P03	3672	3688	ITGA1 ITGB1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0	0.529	0.383	0.676	0.471	0.324	0.617
SL003182	Integrin aVb5	P06756	P11	3685	3693	ITGAV ITGB5	RFU			No	No	DE	0.510	0.517	0.507	0	0	0	0.510	0.300	0.719	0	0	0	0.490	0.281	0.700
SL003183	IP-10	P02778	3627	CXCL10	RFU			No	No	AE	0.528	0.541	0.521	0.528	0.366	0.690	0	0	0	0	0	0	0.472	0.310	0.634
SL003184	sLeptin R	P48357	3953	LEPR	RFU			No	No	AE	0.958	0.976	0.941	0.958	0.939	0.977	0	0	0	0	0	0	0.042	0.023	0.061
SL003186	Lymphotactin	P47992	6375	XCL1	RFU			No	No	DE	0.607	0.692	0.574	0	0	0	0.607	0.387	0.828	0	0	0	0.393	0.172	0.613
SL003187	MDC	O00626	6367	CCL22	RFU			No	No	DE	0.661	0.725	0.625	0	0	0	0.661	0.519	0.803	0	0	0	0.339	0.197	0.481
SL003189	MIP-3b	Q99731	6363	CCL19	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003190	MIP-5	Q16663	6359	CCL15	RFU			No	No	DE	0.636	0.692	0.605	0	0	0	0.636	0.490	0.782	0	0	0	0.364	0.218	0.510
SL003191	P-2	P02775	5473	PPBP	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.345	0.165	0.524	0.655	0.476	0.835
SL003192	Properdin	P27918	5199	CFP	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.420	0.249	0.590	0.580	0.410	0.751
SL003193	6Ckine	O00585	6366	CCL21	RFU			No	No	AE	0.701	0.771	0.660	0.701	0.573	0.829	0	0	0	0	0	0	0.299	0.171	0.427
SL003196	TARC	Q92583	6361	CCL17	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.412	0.242	0.582	0.588	0.418	0.758
SL003197	TECK	O15444	6370	CCL25	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.632	0.510	0.755	0.368	0.245	0.490
SL003198	Tescin	P24821	3371	TNC	RFU			No	No	AE	0.806	0.869	0.762	0.806	0.721	0.891	0	0	0	0	0	0	0.194	0.109	0.279
SL003199	sTie-1	P35590	7075	TIE1	RFU			No	No	DE	0.764	0.843	0.715	0	0	0	0.764	0.650	0.879	0	0	0	0.236	0.121	0.350
SL003200	sTie-2	Q02763	7010	TEK	RFU			No	No	AE	0.538	0.558	0.528	0.538	0.361	0.714	0	0	0	0	0	0	0.462	0.286	0.639
SL003201	VEGF sR2	P35968	3791	KDR	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.560	0.415	0.704	0.440	0.296	0.585
SL003220	C3adesArg	P01024	718	C3	RFU	Calibration Scale		No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL003280	HMG-1	P09429	3146	HMGB1	RFU			No	No	DE	0.750	0.833	0.700	0	0	0	0.750	0.624	0.875	0	0	0	0.250	0.125	0.376
SL003300	HCC-4	O15467	6360	CCL16	RFU			No	No	DCE	0.165	-0.077	0.249	0	0	0	0.165	-0.040	0.370	0.646	0.451	0.841	0.189	0.104	0.273
SL003301	Ck-b-8-1	P55773	6368	CCL23	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.303	0.116	0.490	0.697	0.510	0.884
SL003302	MPIF-1	P55773	6368	CCL23	RFU			No	No	AE	0.749	0.822	0.703	0.749	0.636	0.862	0	0	0	0	0	0	0.251	0.138	0.364
SL003303	CCL28	Q9NRJ3	56477	CCL28	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.360	0.182	0.538	0.640	0.462	0.818
SL003304	IGF-I sR	P08069	3480	IGF1R	RFU			No	No	DE	0.529	0.546	0.521	0	0	0	0.529	0.342	0.716	0	0	0	0.471	0.284	0.658
SL003305	IL-2 sRa	P01589	3559	IL2RA	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003307	IL-2 sRg	P31785	3561	IL2RG	RFU			No	No	ACE	0.423	0.209	0.438	0.423	0.028	0.819	0	0	0	0.371	-0.011	0.752	0.206	0.116	0.297
SL003308	IL-4 sR	P24394	3566	IL4R	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003309	LBP	P18428	3929	LBP	RFU			No	No	AE	0.603	0.647	0.579	0.603	0.451	0.755	0	0	0	0	0	0	0.397	0.245	0.549
SL003310	VEGF121	P15692	7422	VEGFA	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.156	-0.044	0.355	0.844	0.645	1.044
SL003322	VEGF sR3	P35916	2324	FLT4	RFU			No	No	DE	0.849	0.905	0.807	0	0	0	0.849	0.780	0.918	0	0	0	0.151	0.082	0.220
SL003323	PARC	P55774	6362	CCL18	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.641	0.521	0.762	0.359	0.238	0.479
SL003324	Coagulation Factor Xa	P00742	2159	F10	RFU			No	No	DE	0.623	0.685	0.592	0	0	0	0.623	0.455	0.791	0	0	0	0.377	0.209	0.545
SL003326	I-TAC	O14625	6373	CXCL11	RFU			No	No	DE	0.525	0.537	0.519	0	0	0	0.525	0.358	0.691	0	0	0	0.475	0.309	0.642
SL003327	Factor D	P00746	1675	CFD	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003328	Factor I	P05156	3426	CFI	RFU			No	No	AE	0.461	0.437	0.472	0.461	0.272	0.650	0	0	0	0	0	0	0.539	0.350	0.728
SL003329	HCC-1	Q16627	6358	CCL14	RFU			No	No	AE	0.733	0.803	0.690	0.733	0.619	0.848	0	0	0	0	0	0	0.267	0.152	0.381
SL003331	MMP-16	P51512	4325	MMP16	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003332	MMP-17	Q9ULZ9	4326	MMP17	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003334	EMAP-2	Q12904	9255	AIMP1	RFU			No	No	DE	0.868	0.924	0.824	0	0	0	0.868	0.801	0.934	0	0	0	0.132	0.066	0.199
SL003341	Fibrinogen g-chain din	P02679	2266	FGG	RFU			No	No	AE	0.364	0.244	0.408	0.364	0.129	0.599	0	0	0	0	0	0	0.636	0.401	0.871
SL003362	C3d	P01024	718	C3	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003440	PAFAH	Q13093	7941	PLA2G7	RFU			No	No	DE	0.518	0.530	0.513	0	0	0	0.518	0.316	0.720	0	0	0	0.482	0.280	0.684
SL003461	ACTH	P01189	5443	POMC	RFU			No	No	DE	0.416	0.113	0.453	0	0	0	0.416	0.025	0.807	0	0	0	0.584	0.193	0.975
SL003520	calreticulin	P27797	811	CALR	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003522	ERP29	P30040	10961	ERP29	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.436	0.269	0.604	0.564	0.396	0.731
SL003524	Protein disulfide isome	P30101	2923	PDIA3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.527	0.379	0.674	0.473	0.326	0.621
SL003542	NG36	Q96KQ7	10919	EHMT2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.421	0.249	0.594	0.579	0.406	0.751
SL003643	Glutathione S-transfer	P09211	2950	GSTP1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.491	0.335	0.647	0.509	0.353	0.665
SL003647	annexin VI	P08133	309	ANXA6	RFU	Calibration Scale		No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL003648	Rab GDP dissociation	P50395	2665	GDI2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.605	0.475	0.735	0.395	0.265	0.525
SL003653	phosphoglycerate kise	P00558	5230	PGK1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.390	0.216	0.564	0.610	0.436	0.784
SL003655	Transketolase	P29401	7086	TKT	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.626	0.502	0.750	0.374	0.250	0.498
SL003657	Calcineurin	Q08209	P6	5530	5534	PPP3CA PPP3R	RFU			No	No	AE	0.718	0.784	0.677	0.718	0.602	0.834	0	0	0	0	0	0	0.282	0.166	0.398
SL003658	Aflatoxin B1 aldehyde	O43488	8574	AKR7A2	RFU			No	No	DCE	0.240	0.003	0.307	0	0	0	0.240	0.001	0.478	0.548	0.325	0.771	0.212	0.117	0.308
SL003674	BCL2-like 1 protein	Q07817	598	BCL2L1	RFU			No	No	DE	0.452	0.396	0.469	0	0	0	0.452	0.182	0.723	0	0	0	0.548	0.277	0.818
SL003679	IGF-II receptor	P11717	3482	IGF2R	RFU			No	No	DE	0.671	0.735	0.635	0	0	0	0.671	0.536	0.807	0	0	0	0.329	0.193	0.464
SL003680	sRAGE	Q15109	177	AGER	RFU			No	No	AE	0.810	0.868	0.767	0.810	0.730	0.889	0	0	0	0	0	0	0.190	0.111	0.270
SL003685	PBEF	P43490	10135	MPT	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.396	0.224	0.569	0.604	0.431	0.776
SL003687	Nucleoside diphospha	P15531	4830	NME1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003690	RANK	Q9Y6Q6	8792	TNFRSF11A	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003703	BFL1	Q16548	597	BCL2A1	RFU			No	No	DE	0.752	0.834	0.702	0	0	0	0.752	0.629	0.875	0	0	0	0.248	0.125	0.371
SL003711	Caspase-3	P42574	836	CASP3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.546	0.403	0.689	0.454	0.311	0.597
SL003717	Caspase-10	Q92851	843	CASP10	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.385	0.200	0.570	0.615	0.430	0.800

SL003726	Chk2	O96017	11200	CHEK2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003728	cIAP-2	Q13489	330	BIRC3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003733	SMAC	Q9NR28	56616	DIABLO	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003735	4-1BB ligand	P41273	8744	TNFSF9	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003738	B7	P33681	941	CD80	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.475	0.318	0.633	0.525	0.367	0.682
SL003739	DcR3	O95407	8771	TNFRSF6B	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003744	Galectin-3	P17931	3958	LGALS3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.615	0.485	0.744	0.385	0.256	0.515
SL003753	DLC8	P63167	8655	DYNLL1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003761	pTEN	P60484	5728	PTEN	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003764	NCAM-120	P13591	4684	NCAM1	RFU		No	No	AE	0.700	0.768	0.660	0.700	0.573	0.827	0	0	0	0	0	0	0.300	0.173	0.427
SL003770	SARP-2	Q8N474	6422	SFRP1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.490	0.334	0.645	0.510	0.355	0.666
SL003785	GAPDH liver	P04406	2597	GAPDH	RFU		No	No	AE	0.713	0.779	0.673	0.713	0.596	0.831	0	0	0	0	0	0	0.287	0.169	0.404
SL003793	MEK1	Q02750	5604	MAP2K1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.172	-0.027	0.372	0.828	0.628	1.027
SL003800	Kallikrein 4	Q9Y5K2	9622	KLK4	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003803	ERBB4	Q15303	2066	ERBB4	RFU		No	No	DE	0.736	0.846	0.679	0	0	0	0.736	0.577	0.895	0	0	0	0.264	0.105	0.423
SL003849	FGF9	P31371	2254	FGF9	RFU		No	No	DE	0.488	0.445	0.493	0	0	0	0.488	0.100	0.875	0	0	0	0.512	0.125	0.900
SL003862	CD40 ligand soluble	P29965	959	CD40LG	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003863	kallikrein 5	Q9Y337	25818	KLK5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.314	0.126	0.502	0.686	0.498	0.874
SL003872	gp130 soluble	P40189	3572	IL6ST	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.525	0.372	0.678	0.475	0.322	0.628
SL003915	kallikrein 8	O60259	11202	KLK8	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.528	0.379	0.677	0.472	0.323	0.621
SL003916	kallikrein 12	Q9UKR0	43849	KLK12	RFU		No	No	DE	0.399	0.333	0.428	0	0	0	0.399	0.201	0.597	0	0	0	0.601	0.403	0.799
SL003918	kallikrein 13	Q9UKR3	26085	KLK13	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003919	kallikrein 14	Q9P0G3	43847	KLK14	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003930	HPG-	P15428	3248	HPGD	RFU		No	No	DE	0.777	0.868	0.722	0	0	0	0.777	0.653	0.901	0	0	0	0.223	0.099	0.347
SL003951	BDNF	P23560	627	BDNF	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL003970	PTH	P01270	5741	PTH	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003974	Activated Protein C	P04070	5624	PROC	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003990	FGFR-2	P21802	2263	FGFR2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003993	BMP-6	P22004	654	BMP6	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL003994	BMP-1	P13497	649	BMP1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.505	0.350	0.660	0.495	0.340	0.650
SL004008	Proteise-3	P24158	5657	PRTN3	RFU		No	No	DE	0.534	0.552	0.525	0	0	0	0.534	0.360	0.708	0	0	0	0.466	0.292	0.640
SL004009	RAC1	P63000	5879	RAC1	RFU		No	No	DCE	0.242	-0.072	0.314	0	0	0	0.242	-0.027	0.512	0.508	0.258	0.758	0.250	0.140	0.359
SL004010	SCF sR	P10721	3815	KIT	RFU		No	No	DE	0.593	0.636	0.571	0	0	0	0.593	0.436	0.751	0	0	0	0.407	0.249	0.564
SL004015	TAFI	Q96IY4	1361	CPB2	RFU		No	No	AE	0.631	0.688	0.601	0.631	0.480	0.783	0	0	0	0	0	0	0.369	0.217	0.520
SL004016	CXCL16 soluble	Q9H2A7	58191	CXCL16	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.500	0.343	0.657	0.500	0.343	0.657
SL004060	Endothelin-converting	P42892	1889	ECE1	RFU		No	No	AE	0.676	0.738	0.640	0.676	0.546	0.806	0	0	0	0	0	0	0.324	0.194	0.454
SL004063	FGFR-3	P22607	2261	FGFR3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004064	GIB	P04054	5319	PLA2G1B	RFU		No	No	AE	0.353	0.232	0.398	0.353	0.127	0.578	0	0	0	0	0	0	0.647	0.422	0.873
SL004066	GIIE	Q9NZK7	30814	PLA2G2E	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004067	GX	O15496	8399	PLA2G10	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004068	Granzyme B	P10144	3002	GZMB	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004070	Ubiquitin	P62979	6233	RPS27A	RFU		No	No	DE	0.233	-0.096	0.328	0	0	0	0.233	-0.043	0.509	0	0	0	0.767	0.491	1.043
SL004078	BMP-7	P18075	655	BMP7	RFU		No	No	AE	0.620	0.673	0.592	0.620	0.467	0.773	0	0	0	0	0	0	0.380	0.227	0.533
SL004080	BMPR1A	P36894	657	BMPR1A	RFU		No	No	DE	0.395	0.289	0.430	0	0	0	0.395	0.144	0.646	0	0	0	0.605	0.354	0.856
SL004081	Bone proteoglycan II	P07585	1634	DCN	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.449	0.280	0.618	0.551	0.382	0.720
SL004118	TrATPase	P13686	54	ACP5	RFU		No	No	AE	0.698	0.771	0.655	0.698	0.561	0.834	0	0	0	0	0	0	0.302	0.166	0.439
SL004119	discoidin domain rece	Q08345	780	DDR1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004120	Discoidin domain rece	Q16832	4921	DDR2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.146	-0.056	0.348	0.854	0.652	1.056
SL004125	IR	P06213	3643	INSR	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.346	0.165	0.527	0.654	0.473	0.835
SL004126	4-1BB	Q07011	3604	TNFRSF9	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004128	Activin RIB	P36896	91	ACVR1B	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004131	B7-2	P42081	942	CD86	RFU		No	No	DE	0.190	-0.119	0.294	0	0	0	0.190	-0.060	0.440	0	0	0	0.810	0.560	1.060
SL004133	BMP RII	Q13873	659	BMPR2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004134	CD27	P26842	939	CD27	RFU	Calibration Scale	No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL004136	Dtk	Q06418	7301	TYRO3	RFU		No	No	DE	0.586	0.649	0.561	0	0	0	0.586	0.377	0.796	0	0	0	0.414	0.204	0.623
SL004137	EphA1	P21709	2041	EPHA1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.351	0.173	0.530	0.649	0.470	0.827
SL004140	Ephrin-A4	P52798	1945	EF4	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.438	0.269	0.607	0.562	0.393	0.731
SL004141	Ephrin-A5	P52803	1946	EF5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.347	0.166	0.529	0.653	0.471	0.834
SL004142	Ephrin-B3	Q15768	1949	EFNB3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004143	GFRa-2	O00451	2675	GFRA2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.633	0.510	0.757	0.367	0.243	0.490
SL004144	GFRa-3	O60609	2676	GFRA3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004145	HVEM	Q92956	8764	TNFRSF14	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004146	IL-1 R4	Q01638	9173	IL1RL1	RFU		No	No	AE	0.763	0.836	0.715	0.763	0.653	0.872	0	0	0	0	0	0	0.237	0.128	0.347
SL004147	IL-10 Rb	Q08334	3588	IL10RB	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004148	IL-12 Rb1	P42701	3594	IL12RB1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004149	IL-13 Ra1	P78552	3597	IL13RA1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.198	0.001	0.395	0.802	0.605	0.999
SL004151	IL-15 Ra	Q13261	3601	IL15RA	RFU		No	No	DE	0.746	0.847	0.691	0	0	0	0.746	0.601	0.891	0	0	0	0.254	0.109	0.399
SL004152	IL-18 Ra	Q13478	8809	IL18R1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.598	0.466	0.730	0.402	0.270	0.534
SL004153	M-CSF R	P07333	1436	CSF1R	RFU		No	No	AE	0.577	0.612	0.558	0.577	0.418	0.736	0	0	0	0	0	0	0.423	0.264	0.582
SL004154	NCAM-L1	P32004	3897	L1CAM	RFU		No	No	AE	0.578	0.615	0.560	0.578	0.420	0.737	0	0	0	0	0	0	0.422	0.263	0.580
SL004155	PDGF Rb	P09619	5159	PDGFRB	RFU		No	No	AE	0.725	0.791	0.683	0.725	0.610	0.839	0	0	0	0	0	0	0.275	0.161	0.390
SL004156	TRAIL R1	O00220	8797	TNFRSF10A	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004159	TRAIL R4	Q9UBN6	8793	TNFRSF10D	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.494	0.336	0.652	0.506	0.348	0.664
SL004160	TrkB	Q16620	4915	NTRK2	RFU		No	No	AE	0.466	0.445	0.476	0.466	0.273	0.660	0	0	0	0	0	0	0.534	0.340	0.727
SL004180	CD30	P28908	943	TNFRSF8	RFU		No	No	DE	0.637	0.732	0.597	0	0	0	0.637	0.433	0.842	0	0	0	0.363	0.158	0.567
SL004182	GV	P39877	5322	PLA2G5	RFU		No	No	DE	0.779	0.873	0.723	0	0	0	0.779	0.654	0.905	0	0	0	0.221	0.095	0.346
SL004183	P-Cadherin	P22223	1001	CDH3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004208	annexin I	P04083	301	ANXA1	RFU		No	No	AE	0.263	-0.064	0.350	0.263	-0.027	0.554	0	0	0	0	0	0	0.737	0.446	1.027
SL004209	annexin II	P07355	302	ANXA2	RFU		No	No	AE	0.425	0.377	0.446	0.425	0.229	0.622	0	0	0	0	0	0	0.575	0.378	0.771
SL004230	tau	P10636	4137	MAPT	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004253	17-beta-HSD 1	P14061	3292	HSD17B1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004258	Adiponectin	Q15848	9370	ADIPOQ	RFU		No	No	AE	0.720	0.793	0.676	0.720	0.595	0.845	0	0	0	0	0	0	0.280	0.155	0.405
SL004260	resistin	Q9HD89	56729	RETN	RFU		No	No	AE	0.561	0.594	0.545	0.561	0.388	0.734	0	0	0	0	0	0	0.439	0.266	0.612
SL004271	GFAP	P14136	2670	GFAP	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004296	Myokise human	P00568	203	AK1	RFU		No	No	AE	0.552	0.579	0.539	0.552	0.380	0.724	0	0	0	0	0	0	0.448	0.276	0.620
SL004297	NEUREGULIN-1	Q02297	3084	NRG1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.372	0.193	0.551	0.628	0.449	0.807
SL004298	granzyme A	P12544	3001	GZMA	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.161	-0.040	0.361	0.839	0.639	1.040
SL004299	Livin B	Q96CA5	79444	BIRC7	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004301	Ku70	P12956	2547	XRCC6	RFU		No	No	DE	0.353	0.192	0.404	0	0	0	0.353	0.092	0.615	0	0	0	0.647	0.385	0.908
SL004304	STX1a	Q16623	6804	STX1A	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004305	Topoisomerase I	P11387	7150	TOP1	RFU		No	No	DE	0.716	0.804	0.668	0	0	0	0.716	0.571	0.861	0	0	0	0.284	0.139	0.429
SL004306	UBC9	P63279	7329	UBE2I	RFU		No	No	AE	0.698	0.765	0.658	0.698	0.572	0.825	0	0	0	0	0	0	0.302	0.175	0.428
SL004326	TNFSF18	Q9UNG2	8995	TNFSF18	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1

SL004327	BAFF	Q9Y275	10673	TNFSF13B	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.299	0.110	0.487	0.701	0.513	0.890
SL004329	BMP-14	P43026	8200	GDF5	RFU		No	No	DE	0.445	0.370	0.465	0	0	0	0.445	0.158	0.731	0	0	0	0.555	0.269	0.842
SL004330	CD22	P20273	933	CD22	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004331	CNTF	P26441	1270	CNTF	RFU		No	No	DE	0.499	0.498	0.500	0	0	0	0.499	0.182	0.816	0	0	0	0.501	0.184	0.818
SL004332	EG-VEGF	P58294	84432	PROK1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004333	FGF-10	O15520	2255	FGF10	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004334	FGF-16	O43320	8823	FGF16	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.585	0.450	0.719	0.415	0.281	0.550
SL004335	FGF-17	O60258	8822	FGF17	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004336	FGF-18	O76093	8817	FGF18	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004337	FGF-19	O95750	9965	FGF19	RFU		No	No	AE	0.554	0.583	0.540	0.554	0.381	0.727	0	0	0	0	0	0	0.446	0.273	0.619
SL004338	FGF-20	Q9NP95	26281	FGF20	RFU		No	No	AE	0.707	0.789	0.661	0.707	0.565	0.849	0	0	0	0	0	0	0.293	0.151	0.435
SL004339	FGF-5	P12034	2250	FGF5	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004340	FGF-6	P10767	2251	FGF6	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.401	0.228	0.573	0.599	0.427	0.772
SL004342	FGF-8B	P55075	2253	FGF8	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004343	Flt3 ligand	P49771	2323	FLT3LG	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004345	GDF-11	O95390	10220	GDF11	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004346	IL-20	Q9NYY1	50604	IL20	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004347	IL-22	Q9GZX6	50616	IL22	RFU		No	No	DE	0.474	0.451	0.482	0	0	0	0.474	0.239	0.708	0	0	0	0.526	0.292	0.761
SL004348	IFN-lambda 1	Q8IU54	282618	IL29	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.529	0.381	0.677	0.471	0.323	0.619
SL004349	IFN-lambda 2	Q8IZJ0	282616	IL28A	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004350	IL-17B	Q9UHF5	27190	IL17B	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004351	IL-17E	Q9H293	64806	IL25	RFU		No	No	DE	0.434	0.348	0.458	0	0	0	0.434	0.150	0.719	0	0	0	0.566	0.281	0.850
SL004352	IL-17F	Q96PD4	112744	IL17F	RFU		No	No	DE	0.628	0.726	0.589	0	0	0	0.628	0.410	0.845	0	0	0	0.372	0.155	0.590
SL004353	IL-17D	Q8TAD2	53342	IL17D	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004354	IL-19	Q9UHD0	29949	IL19	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.543	0.396	0.690	0.457	0.310	0.604
SL004355	LD78-beta	P16619	414062	CCL3L1	RFU		No	No	DE	0.595	0.679	0.565	0	0	0	0.595	0.360	0.830	0	0	0	0.405	0.170	0.640
SL004356	LAG-1	Q8NHW4	388372	CCL4L1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.188	-0.009	0.384	0.812	0.616	1.009
SL004359	Neurotrophin-3	P20783	4908	NTF3	RFU		No	No	DE	0.640	0.725	0.602	0	0	0	0.640	0.451	0.829	0	0	0	0.360	0.171	0.549
SL004360	Neurotrophin-5	P34130	4909	NTF4	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004362	SCGF-beta	Q9Y240	6320	CLEC11A	RFU		No	No	AE	0.613	0.661	0.587	0.613	0.464	0.763	0	0	0	0	0	0	0.387	0.237	0.536
SL004363	SCGF-alpha	Q9Y240	6320	CLEC11A	RFU		No	No	AE	0.737	0.805	0.693	0.737	0.625	0.849	0	0	0	0	0	0	0.263	0.151	0.375
SL004364	TACI	O14836	23495	TNFRSF13B	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.246	0.047	0.445	0.754	0.555	0.953
SL004365	TWEAK	O43508	8742	TNFSF12	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004366	TWEAKR	Q9NP84	51330	TNFRSF12A	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004367	DKK1	O94907	22943	DKK1	RFU		No	No	AE	0.547	0.577	0.534	0.547	0.355	0.739	0	0	0	0	0	0	0.453	0.261	0.645
SL004400	Coagulation Factor IX	P00740	2158	F9	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.438	0.267	0.609	0.562	0.391	0.733
SL004415	ACE2	Q9BYF1	59272	ACE2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004438	Cystatin M	Q15828	1474	CST6	RFU		No	No	AE	0.755	0.825	0.710	0.755	0.647	0.862	0	0	0	0	0	0	0.245	0.138	0.353
SL004457	Protease nexin I	P07093	5270	SERPINE2	RFU		No	No	DE	0.325	0.171	0.381	0	0	0	0.325	0.091	0.559	0	0	0	0.675	0.441	0.909
SL004458	Elafin	P19957	5266	PI3	RFU		No	No	AE	0.476	0.460	0.482	0.476	0.280	0.671	0	0	0	0	0	0	0.524	0.329	0.720
SL004466	Heparin cofactor II	P05546	3053	SERPIND1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.458	0.293	0.623	0.542	0.377	0.707
SL004469	amyloid precursor prot	P05067	351	APP	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.388	0.214	0.561	0.612	0.439	0.786
SL004477	calgranulin B	P06702	6280	S100A9	RFU		No	No	DE	0.463	0.440	0.474	0	0	0	0.463	0.267	0.660	0	0	0	0.537	0.340	0.733
SL004482	Endoglin	P17813	2022	ENG	RFU		No	No	AE	0.485	0.476	0.489	0.485	0.294	0.676	0	0	0	0	0	0	0.515	0.324	0.706
SL004484	SP-D	P35247	6441	SFTPD	RFU		No	No	DE	0.597	0.669	0.568	0	0	0	0.597	0.384	0.810	0	0	0	0.403	0.190	0.616
SL004486	VEGF-C	P49767	7424	VEGFC	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.229	0.032	0.425	0.771	0.575	0.968
SL004492	TLR2	O60603	7097	TLR2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.332	0.147	0.516	0.668	0.484	0.853
SL004511	BPI	P17213	671	BPI	RFU		No	No	DE	0.612	0.663	0.585	0	0	0	0.612	0.456	0.768	0	0	0	0.388	0.232	0.544
SL004515	PGRP-S	O75594	8993	PGLYRP1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.313	0.130	0.497	0.687	0.503	0.870
SL004516	MBL	P11226	4153	MBL2	RFU		No	No	AE	0.813	0.873	0.770	0.813	0.733	0.893	0	0	0	0	0	0	0.187	0.107	0.267
SL004536	LEAP-1	P81172	57817	HAMP	RFU		No	No	DE	0.224	-0.004	0.310	0	0	0	0.224	-0.002	0.450	0	0	0	0.776	0.550	1.002
SL004556	DAF	P08174	1604	CD55	RFU		No	No	AE	0.590	0.628	0.569	0.590	0.441	0.739	0	0	0	0	0	0	0.410	0.261	0.559
SL004579	Macrophage mannose	P22897	4360	MRC1	RFU		No	No	AE	0.784	0.852	0.738	0.784	0.687	0.881	0	0	0	0	0	0	0.216	0.119	0.313
SL004580	Macrophage scavenge	P21757	4481	MSR1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004588	IL-1 R AcP	Q9NPH3	3556	IL1RAP	RFU		No	No	AE	0.806	0.866	0.762	0.806	0.723	0.888	0	0	0	0	0	0	0.194	0.112	0.277
SL004589	Azurocidin	P20160	566	AZU1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.542	0.397	0.687	0.458	0.313	0.603
SL004591	G-CSF-R	Q99062	1441	CSF3R	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.171	-0.027	0.369	0.829	0.631	1.027
SL004605	40S ribosomal protein	P08865	3921	RPSA	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004610	LRP8	Q14114	7804	LRP8	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.414	0.243	0.586	0.586	0.414	0.757
SL004625	ADAMTS-4	O75173	9507	ADAMTS4	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.351	0.166	0.535	0.649	0.465	0.834
SL004626	ADAMTS-5	Q9U0	11096	ADAMTS5	RFU		No	No	DE	0.832	0.901	0.783	0	0	0	0.832	0.746	0.918	0	0	0	0.168	0.082	0.254
SL004635	CD30 Ligand	P32971	944	TNFSF8	RFU		No	No	AE	0.690	0.760	0.649	0.690	0.555	0.825	0	0	0	0	0	0	0.310	0.175	0.445
SL004636	Flt-3	P36888	2322	FLT3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.625	0.500	0.750	0.375	0.250	0.500
SL004637	MSP R	Q04912	4486	MST1R	RFU		No	No	DE	0.482	0.443	0.490	0	0	0	0.482	0.138	0.827	0	0	0	0.518	0.173	0.862
SL004639	TrkC	Q16288	4916	NTRK3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.498	0.343	0.653	0.502	0.347	0.657
SL004642	ADAM 9	Q13443	8754	ADAM9	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004643	Angiopoietin-4	Q9Y264	51378	ANGPT4	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.361	0.182	0.540	0.639	0.460	0.818
SL004644	EDA	Q92838	1896	EDA	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004645	HAI-1	O43278	6692	SPINT1	RFU		No	No	DE	0.539	0.564	0.529	0	0	0	0.539	0.350	0.729	0	0	0	0.461	0.271	0.650
SL004646	Layilin	Q6UX15	143903	LAYN	RFU		No	No	AE	0.337	0.168	0.392	0.337	0.083	0.591	0	0	0	0	0	0	0.663	0.409	0.917
SL004648	LIGHT	O43557	8740	TNFSF14	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004649	OX40 Ligand	P23510	7292	TNFSF4	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004650	sFRP-3	Q92765	2487	FRZB	RFU		No	No	DE	0.326	0.141	0.385	0	0	0	0.326	0.069	0.583	0	0	0	0.674	0.417	0.931
SL004652	WIF-1	Q9Y5W5	11197	WIF1	RFU		No	No	DE	0.231	0.019	0.313	0	0	0	0.231	0.011	0.451	0	0	0	0.769	0.549	0.989
SL004654	Granzyme H	P20718	2999	GZMH	RFU		No	No	DE	0.251	-0.009	0.335	0	0	0	0.251	-0.005	0.506	0	0	0	0.749	0.494	1.005
SL004660	BSP	P21815	3381	IBSP	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.387	0.214	0.561	0.613	0.439	0.786
SL004661	Aggrecan	P16112	176	ACAN	RFU		No	No	AE	0.384	0.278	0.421	0.384	0.146	0.621	0	0	0	0	0	0	0.616	0.379	0.854
SL004668	Apo E3	P02649	348	APOE	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.640	0.520	0.761	0.360	0.239	0.480
SL004669	Apo E4	P02649	348	APOE	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.710	0.609	0.811	0.290	0.189	0.391
SL004670	Artemin	Q5T4W7	9048	ARTN	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004671	BAFF Receptor	Q96RJ3	115650	TNFRSF13C	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.400	0.228	0.573	0.600	0.427	0.772
SL004672	BCMA	Q02223	608	TNFRSF17	RFU		No	No	AE	0.706	0.767	0.668	0.706	0.594	0.819	0	0	0	0	0	0	0.294	0.181	0.406
SL004673	Cathepsin S	P25774	1520	CTSS	RFU		No	No	DE	0.521	0.534	0.515	0	0	0	0.521	0.331	0.712	0	0	0	0.479	0.288	0.669
SL004676	IGFBP-5	P24593	3488	IGFBP5	RFU		No	No	AE	0.239	0.019	0.321	0.239	0.010	0.467	0	0	0	0	0	0	0.761	0.533	0.990
SL004683	Noggin	Q13253	9241	NOG	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004685	Persephin	O60542	5623	PSPN	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.152	-0.051	0.354	0.848	0.646	1.051
SL004686	TNFSF15	O95150	9966	TNFSF15	RFU		No	No	AE	0.544	0.570	0.532	0.544	0.353	0.734	0	0	0	0	0	0	0.456	0.266	0.647
SL004687	TSLP	Q969D9	85480	TSLP	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004689	WISP-1	O95388	8840	WISP1	RFU		No	No	DE	0.275	0.057	0.350	0	0	0	0.275	0.029	0.522	0	0	0	0.725	0.478	0.971
SL004692	CLF-1/CLC Complex	O75462 Q9U	9244 2352	CRLF1 CLCF1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004697	HPV E7 Type 16	P03129	1489079	Human-virus	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004698	HPV E7 Type18	P06788	1489089	Human-virus	RFU		No	No	AE	0.511	0.517	0.508	0.511	0.328	0.695	0	0	0	0	0	0	0.489	0.305	0.672
SL004704	COMMD7	Q86VX2	149951	COMMD7	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.269	0.077	0.460	0.731	0.540	0.923

SL004708	CTAP-III	P02775	5473	PPBP	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.367	0.191	0.543	0.633	0.457	0.809
SL004712	SDF-1	P48061	6387	CXCL12	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.409	0.233	0.584	0.591	0.416	0.767
SL004714	LIF sR	P42702	3977	LIFR	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004716	JNK2	P45984	5601	MAPK9	RFU			No	No	DE	0.696	0.784	0.650	0	0	0	0.696	0.541	0.851	0	0	0	0.304	0.149	0.459
SL004718	Karyopherin-a2	P52292	3838	KP2	RFU			No	No	AE	0.251	-0.009	0.335	0.251	-0.005	0.506	0	0	0	0	0	0	0.749	0.494	1.005
SL004720	Calcineurin B a	P63098	5534	PPP3R1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004723	HDAC8	Q9BY41	55869	HDAC8	RFU			No	No	AE	0.518	0.530	0.513	0.518	0.323	0.713	0	0	0	0	0	0	0.482	0.287	0.677
SL004724	MOZ	Q92794	7994	KAT6A	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004725	Hat1	O14929	8520	HAT1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004726	CD97	P48960	976	CD97	RFU			No	No	DE	0.245	-0.121	0.340	0	0	0	0.245	-0.050	0.540	0	0	0	0.755	0.460	1.050
SL004737	Tropomyosin 1 alpha c	P09493	7168	TPM1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004739	ITI heavy chain H4	Q14624	3700	ITIH4	RFU			No	No	AE	0.779	0.844	0.735	0.779	0.685	0.873	0	0	0	0	0	0	0.221	0.127	0.315
SL004742	Afamin	P43652	173	AFM	RFU			No	No	AE	0.463	0.437	0.474	0.463	0.259	0.667	0	0	0	0	0	0	0.537	0.333	0.741
SL004750	DEAD-box protein 19E	Q9UMR2	11269	DDX19B	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004751	HO-2	P30519	3163	HMOX2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004752	DRR1	O95990	11170	FAM107A	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004757	DRG-1	Q9NP79	51534	VTA1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.569	0.431	0.707	0.431	0.293	0.569
SL004759	eIF-5	P55010	1983	EIF5	RFU			No	No	DE	0.822	0.894	0.773	0	0	0	0.822	0.731	0.913	0	0	0	0.178	0.087	0.269
SL004760	PAFAH beta subunit	P68402	5049	PAFAH1B2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.642	0.521	0.763	0.358	0.237	0.479
SL004765	MAPKAPK3	Q16644	7867	MAPKAPK3	RFU			No	No	AE	0.734	0.806	0.690	0.734	0.618	0.851	0	0	0	0	0	0	0.266	0.149	0.382
SL004768	AIF1	P55008	199	AIF1	RFU			No	No	AE	0.387	0.301	0.421	0.387	0.172	0.602	0	0	0	0	0	0	0.613	0.398	0.828
SL004771	Aurora kise A	O14965	6790	AURKA	RFU			No	No	DE	0.500	0.500	0.500	0	0	0	0.500	0.260	0.739	0	0	0	0.500	0.261	0.740
SL004781	CSK	P41240	1445	CSK	RFU			No	No	AE	0.753	0.817	0.710	0.753	0.651	0.855	0	0	0	0	0	0	0.247	0.145	0.349
SL004782	TSG-6	P98066	7130	TNFAIP6	RFU			No	No	AE	0.656	0.714	0.623	0.656	0.522	0.791	0	0	0	0	0	0	0.344	0.209	0.478
SL004791	DR3	Q93038	8718	TNFRSF25	RFU			No	No	DE	0.880	0.927	0.843	0	0	0	0.880	0.826	0.935	0	0	0	0.120	0.065	0.174
SL004795	ERAB	Q99714	3028	HSD17B10	RFU			No	No	DCE	0.230	-0.053	0.303	0	0	0	0.230	-0.022	0.481	0.539	0.305	0.772	0.232	0.129	0.335
SL004804	Nectin-like protein 1	Q8N126	57863	CADM3	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004805	Nectin-like protein 2	Q9BY67	23705	CADM1	RFU			No	No	DE	0.383	0.278	0.421	0	0	0	0.383	0.146	0.620	0	0	0	0.617	0.380	0.854
SL004812	Triosephosphate isom	P60174	7167	TPI1	RFU			No	No	ACE	0.374	-0.437	0.412	0.374	-0.039	0.787	0	0	0	0.371	-0.014	0.756	0.256	0.144	0.368
SL004814	Coactosin-like protein	Q14019	23406	COTL1	RFU			No	No	DE	0.545	0.587	0.530	0	0	0	0.545	0.304	0.787	0	0	0	0.455	0.213	0.696
SL004820	Phosphoglycerate mut	P18669	5223	PGAM1	RFU	Calibration Scale		No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL004823	Cyclophilin A	P62937	5478	PPIA	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.601	0.470	0.732	0.399	0.268	0.530
SL004837	Activin AB	P08476 P09	3624 3625	INHBA INHBB	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.389	0.215	0.563	0.611	0.437	0.785
SL004844	EphA5	P54756	2044	EPHA5	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004845	EphB4	P54760	2050	EPHB4	RFU			No	No	DE	0.289	0.146	0.350	0	0	0	0.289	0.087	0.492	0	0	0	0.711	0.508	0.913
SL004849	IL-1 sR9	Q9NP60	26280	IL1RAPL2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004850	IL-17 sR	Q96F46	23765	IL17RA	RFU			No	No	DE	0.936	0.962	0.912	0	0	0	0.936	0.907	0.965	0	0	0	0.064	0.035	0.093
SL004851	ALK-1	P37023	94	ACVRL1	RFU			No	No	DE	0.563	0.668	0.539	0	0	0	0.563	0.252	0.875	0	0	0	0.437	0.125	0.748
SL004852	B7-H1	Q9NZQ7	29126	CD274	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.152	-0.047	0.351	0.848	0.649	1.047
SL004853	B7-H2	O75144	23308	ICOSLG	RFU			No	No	AE	0.472	0.455	0.480	0.472	0.279	0.665	0	0	0	0	0	0	0.528	0.335	0.721
SL004855	contactin-1	Q12860	1272	CNTN1	RFU			No	No	AE	0.464	0.439	0.475	0.464	0.256	0.672	0	0	0	0	0	0	0.536	0.328	0.744
SL004856	Desmoglein-1	Q02413	1828	DSG1	RFU			No	No	AE	0.262	-0.182	0.356	0.262	-0.064	0.587	0	0	0	0	0	0	0.738	0.413	1.064
SL004857	Desmoglein-2	Q14126	1829	DSG2	RFU			No	No	DE	0.618	0.673	0.590	0	0	0	0.618	0.461	0.776	0	0	0	0.382	0.224	0.539
SL004858	GFRa-1	P56159	2674	GFRA1	RFU	Calibration Scale		No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL004859	GITR	Q9Y5U5	8784	TNFRSF18	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004860	HTRA2	O43464	27429	HTRA2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.371	0.194	0.548	0.629	0.452	0.806
SL004861	IL-18 Rb	O95256	8807	IL18RAP	RFU			No	No	DE	0.794	0.880	0.740	0	0	0	0.794	0.680	0.908	0	0	0	0.206	0.092	0.320
SL004862	PD-L2	Q9BQ51	80380	PDCD1LG2	RFU			No	No	DE	0.584	0.639	0.560	0	0	0	0.584	0.385	0.783	0	0	0	0.416	0.217	0.615
SL004863	TAJ	Q9NS68	55504	TNFRSF19	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004864	Cadherin-12	P55289	1010	CDH12	RFU			No	No	DE	0.300	-0.176	0.383	0	0	0	0.300	-0.052	0.653	0	0	0	0.700	0.347	1.052
SL004865	Cadherin-6	P55285	1004	CDH6	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004866	Carbonic anhydrase I	P00915	759	CA1	RFU			No	No	AE	0.551	0.578	0.538	0.551	0.379	0.723	0	0	0	0	0	0	0.449	0.277	0.621
SL004867	Carbonic anhydrase III	P07451	761	CA3	RFU			No	No	AE	0.591	0.633	0.569	0.591	0.433	0.748	0	0	0	0	0	0	0.409	0.252	0.567
SL004868	Carbonic anhydrase V	P43166	766	CA7	RFU			No	No	DE	0.389	0.111	0.435	0	0	0	0.389	0.032	0.746	0	0	0	0.611	0.254	0.968
SL004869	Carbonic anhydrase X	Q8N1Q1	377677	CA13	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.498	0.344	0.651	0.502	0.349	0.656
SL004871	DR6	O75509	27242	TNFRSF21	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.538	0.390	0.686	0.462	0.314	0.610
SL004872	EDAR	Q9UNE0	10913	EDAR	RFU			No	No	AE	0.765	0.829	0.722	0.765	0.668	0.862	0	0	0	0	0	0	0.235	0.138	0.332
SL004875	IL-1Rrp2	Q9HB29	8808	IL1RL2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.286	0.094	0.478	0.714	0.522	0.906
SL004876	Kallistatin	P29622	5267	SERPI4	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.487	0.325	0.650	0.513	0.350	0.675
SL004891	hnRNP A2/B1	P22626	3181	HNRNPA2B1	RFU			No	No	DE	0.723	0.809	0.674	0	0	0	0.723	0.583	0.862	0	0	0	0.277	0.138	0.417
SL004899	HSP70 protein 8	P11142	3312	HSPA8	RFU			No	No	DE	0.548	0.613	0.530	0	0	0	0.548	0.261	0.835	0	0	0	0.452	0.165	0.739
SL004901	Protein disulfide-isome	P07237	5034	P4HB	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004908	Tropomyosin 2	P07951	7169	TPM2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004914	PPase	Q15181	5464	PPA1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004915	NCC27	O00299	1192	CLIC1	RFU			No	No	AE	0.745	0.809	0.702	0.745	0.640	0.849	0	0	0	0	0	0	0.255	0.151	0.360
SL004919	Peroxiredoxin-1	Q06830	5052	PRDX1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.517	0.367	0.667	0.483	0.333	0.633
SL004920	Cofilin-1	P23528	1072	CFL1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.624	0.499	0.750	0.376	0.250	0.501
SL004921	NDP kise B	P22392	4831	NME2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.560	0.420	0.700	0.440	0.300	0.580
SL004925	AGR2	O95994	10551	AGR2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004932	Peroxiredoxin-5	P30044	25824	PRDX5	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004938	CaMKK alpha	Q8N5S9	84254	CAMKK1	RFU			No	No	DE	0.383	0.293	0.418	0	0	0	0.383	0.165	0.601	0	0	0	0.617	0.399	0.835
SL004939	PTP-1B	P18031	5770	PTPN1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL004940	PTP-1C	P29350	5777	PTPN6	RFU			No	No	ACE	0.275	-0.378	0.353	0.275	-0.080	0.631	0	0	0	0.498	0.166	0.830	0.227	0.127	0.327
SL005034	RAN	P62826	5901	RAN	RFU			No	No	AE	0.616	0.667	0.589	0.616	0.463	0.769	0	0	0	0	0	0	0.384	0.231	0.537
SL005059	TGF-b R III	Q03167	7049	TGFBR3	RFU			No	No	AE	0.544	0.568	0.533	0.544	0.372	0.717	0	0	0	0	0	0	0.456	0.283	0.628
SL005084	Periostin	Q15063	10631	POSTN	RFU			No	No	DE	0.396	0.313	0.428	0	0	0	0.396	0.174	0.617	0	0	0	0.604	0.383	0.826
SL005087	IGFBP-7	Q16270	3490	IGFBP7	RFU			No	No	AE	0.446	0.405	0.463	0.446	0.229	0.664	0	0	0	0	0	0	0.554	0.336	0.771
SL005102	SHBG	P04278	6462	SHBG	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.370	0.194	0.547	0.630	0.453	0.806
SL005115	Spondin-1	Q9HCB6	10418	SPON1	RFU			No	No	DE	0.514	0.522	0.510	0	0	0	0.514	0.334	0.695	0	0	0	0.486	0.305	0.666
SL005152	TIG2	Q99969	5919	RARRES2	RFU			No	No	DE	0.615	0.681	0.584	0	0	0	0.615	0.431	0.799	0	0	0	0.385	0.201	0.569
SL005153	CNTFR alpha	P26992	1271	CNTFR	RFU			No	No	AE	0.551	0.580	0.538	0.551	0.374	0.729	0	0	0	0	0	0	0.449	0.271	0.626
SL005155	Cripto	P13385	6997	TDGF1	RFU			No	No	DE	0.538	0.588	0.524	0	0	0	0.538	0.252	0.823	0	0	0	0.462	0.177	0.748
SL005156	DAN	P41271	4681	NBL1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.539	0.393	0.685	0.461	0.315	0.607
SL005157	DC-SIGN	Q9NNX6	30835	CD209	RFU			No	No	AE	0.559	0.589	0.544	0.559	0.388	0.729	0	0	0	0	0	0	0.441	0.271	0.612
SL005158	DC-SIGNR	Q9H2X3	10332	CLEC4M	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.348	0.161	0.535	0.652	0.465	0.839
SL005159	EPO-R	P19235	2057	EPOR	RFU			No	No	DE	0.843	0.909	0.795	0	0	0	0.843	0.762	0.923	0	0	0	0.157	0.077	0.238
SL005160	ESAM	Q96AP7	90952	ESAM	RFU			No	No	AE	0.692	0.759	0.653	0.692	0.563	0.821	0	0	0	0	0	0	0.308	0.179	0.437
SL005161	FGF-12	P61328	2257	FGF12	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005164	Galectin-2	P05162	3957	LGALS2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005165	Galectin-4	P56470	3960	LGALS4	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.147	-0.056	0.349	0.853	0.651	1.056
SL005167	Galectin-8	O00214	3964	LGALS8	RFU			No	No	DE	0.695	0.809	0.643	0	0	0	0.695	0.511	0.879	0	0	0	0.305	0.121	0.489
SL005168	Growth hormone recep	P10912	2690	GHR	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.609	0.479	0.738	0.391	0.262	0.521
SL005169	sICAM-5	Q9UMF0	7087	ICAM5	RFU			No	No	AE	0.766	0.830	0.722	0.766	0.668	0.864	0	0	0	0	0	0	0.234	0.136	0.332

SL005170	ICOS	Q9Y6W8	29851	ICOS	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005171	IGFBP-4	P22692	3487	IGFBP4	RFU		No	No	AE	0.615	0.666	0.588	0.615	0.462	0.769	0	0	0	0	0	0	0.385	0.231	0.538
SL005172	IGFBP-6	P24592	3489	IGFBP6	RFU		No	No	AE	0.393	0.318	0.424	0.393	0.186	0.600	0	0	0	0	0	0	0.607	0.400	0.814
SL005174	IL-17B R	Q9NRM6	55540	IL17RB	RFU		No	No	AE	0.356	0.244	0.399	0.356	0.138	0.574	0	0	0	0	0	0	0.644	0.426	0.862
SL005178	IL-1F7	Q9NZH6	27178	IL1F7	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005181	IL-20 Ra	Q9UHF4	53832	IL20RA	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005183	IL-22BP	Q969J5	116379	IL22RA2	RFU		No	No	AE	0.531	0.550	0.523	0.531	0.347	0.716	0	0	0	0	0	0	0.469	0.284	0.653
SL005184	IL-23	P29460	Q9I	3593 5156	IL12B IL23A	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005185	IL-23 R	Q5VWK5	149233	IL23R	RFU		No	No	AE	0.660	0.739	0.620	0.660	0.495	0.826	0	0	0	0	0	0	0.340	0.174	0.505
SL005187	IL-3 Ra	P26951	3563	IL3RA	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.424	0.255	0.592	0.576	0.408	0.745
SL005188	IL-5 Ra	Q01344	3568	IL5RA	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.519	0.369	0.669	0.481	0.331	0.631
SL005189	IL-7 Ra	P16871	3575	IL7R	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005190	ILT-2	Q8NHL6	10859	LILRB1	RFU		No	No	AE	0.830	0.887	0.788	0.830	0.756	0.904	0	0	0	0	0	0	0.170	0.096	0.244
SL005191	ILT-4	Q8N423	10288	LILRB2	RFU		No	No	AE	0.797	0.862	0.752	0.797	0.707	0.887	0	0	0	0	0	0	0.203	0.113	0.293
SL005193	JAM-B	P57087	58494	JAM2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005194	JAM-C	Q9BX67	83700	JAM3	RFU		No	No	DCE	0.232	-0.034	0.304	0	0	0	0.232	-0.014	0.478	0.556	0.321	0.790	0.212	0.119	0.306
SL005195	LAG-3	P18627	3902	LAG3	RFU		No	No	AE	0.637	0.696	0.605	0.637	0.485	0.789	0	0	0	0	0	0	0.363	0.211	0.515
SL005196	LSAMP	Q13449	4045	LSAMP	RFU		No	No	AE	0.594	0.638	0.572	0.594	0.437	0.752	0	0	0	0	0	0	0.406	0.248	0.563
SL005197	LIMP II	Q14108	950	SCARB2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005199	MICA	Q29983	4276	MICA	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.504	0.352	0.657	0.496	0.343	0.648
SL005200	MICB	Q29980	4277	MICB	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.366	0.188	0.543	0.634	0.457	0.812
SL005201	MIS	P03971	268	AMH	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.313	0.120	0.506	0.687	0.494	0.880
SL005202	MSP	P26927	4485	MST1	RFU		No	No	AE	0.938	0.964	0.914	0.938	0.909	0.966	0	0	0	0	0	0	0.062	0.034	0.091
SL005204	NKG2D	P26718	22914	KLRK1	RFU		No	No	AE	0.579	0.637	0.555	0.579	0.365	0.792	0	0	0	0	0	0	0.421	0.208	0.635
SL005205	NKp30	O14931	259197	NCR3	RFU		No	No	DE	0.865	0.924	0.821	0	0	0	0.865	0.797	0.934	0	0	0	0.135	0.066	0.203
SL005206	NKp44	O95944	9436	NCR2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005207	NKp46	O76036	9437	NCR1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005208	Nogo Receptor	Q9BZR6	65078	RTN4R	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.517	0.366	0.668	0.483	0.332	0.634
SL005209	Notch-3	Q9UM47	4854	NOTCH3	RFU		No	No	AE	0.374	0.275	0.412	0.374	0.154	0.593	0	0	0	0	0	0	0.626	0.407	0.846
SL005210	Nr-CAM	Q92823	4897	NRCAM	RFU		No	No	AE	0.502	0.504	0.502	0.502	0.308	0.696	0	0	0	0	0	0	0.498	0.304	0.692
SL005212	Prolactin Receptor	P16471	5618	PRLR	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005213	RELT	Q969Z4	84957	RELT	RFU		No	No	AE	0.679	0.761	0.636	0.679	0.521	0.837	0	0	0	0	0	0	0.321	0.163	0.479
SL005214	Semaphorin-6A	Q9H2E6	57556	SEMA6A	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.452	0.288	0.615	0.548	0.385	0.712
SL005215	Siglec-3	P20138	945	CD33	RFU		No	No	DE	0.902	0.941	0.870	0	0	0	0.902	0.858	0.946	0	0	0	0.098	0.054	0.142
SL005217	Siglec-6	O43699	946	SIGLEC6	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.287	0.100	0.475	0.713	0.525	0.900
SL005218	Siglec-7	Q9Y286	27036	SIGLEC7	RFU		No	No	AE	0.570	0.605	0.552	0.570	0.401	0.739	0	0	0	0	0	0	0.430	0.261	0.599
SL005219	Siglec-9	Q9Y336	27180	SIGLEC9	RFU		No	No	AE	0.996	0.998	0.994	0.996	0.994	0.998	0	0	0	0	0	0	0.004	0.002	0.006
SL005220	Sonic Hedgehog	Q15465	6469	SHH	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.422	0.253	0.592	0.578	0.408	0.747
SL005221	SREC-I	Q14162	8578	SCARF1	RFU		No	No	AE	0.559	0.591	0.544	0.559	0.384	0.734	0	0	0	0	0	0	0.441	0.266	0.616
SL005222	SREC-II	Q96GP6	91179	SCARF2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005223	TCCR	Q6UWB1	9466	IL27RA	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.148	-0.054	0.350	0.852	0.650	1.054
SL005224	Thrombopoietin Recep	P40238	4352	MPL	RFU		No	No	DE	0.630	0.720	0.592	0	0	0	0.630	0.426	0.835	0	0	0	0.370	0.165	0.574
SL005225	TrkA	P04629	4914	NTRK1	RFU		No	No	AE	0.186	-0.095	0.286	0.186	-0.050	0.422	0	0	0	0	0	0	0.814	0.578	1.050
SL005226	TSLP R	Q9HC73	64109	CRLF2	RFU		No	No	DE	0.299	-0.028	0.376	0	0	0	0.299	-0.011	0.609	0	0	0	0.701	0.391	1.011
SL005227	ULBP-1	Q9BZM6	80329	ULBP1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005228	ULBP-2	Q9BZM5	80328	ULBP2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005229	ULBP-3	Q9BZM4	79465	ULBP3	RFU		No	No	AE	0.763	0.828	0.719	0.763	0.664	0.862	0	0	0	0	0	0	0.237	0.138	0.336
SL005230	UNC5H3	O95185	8633	UNC5C	RFU		No	No	AE	0.473	0.458	0.480	0.473	0.294	0.651	0	0	0	0	0	0	0.527	0.349	0.706
SL005231	UNC5H4	Q6UXZ4	137970	UNC5D	RFU		No	No	DE	0.493	0.488	0.495	0	0	0	0.493	0.301	0.685	0	0	0	0.507	0.315	0.699
SL005233	XEDAR	Q9HAV5	60401	EDA2R	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005234	GDF-9	O60383	2661	GDF9	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005235	NOG	Q9H9S0	79923	NOG	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005236	NovH	P48745	4856	NOV	RFU		No	No	DE	0.235	-0.014	0.321	0	0	0	0.235	-0.007	0.477	0	0	0	0.765	0.523	1.007
SL005250	Chymase	P23946	1215	CMA1	RFU		No	No	DE	0.502	0.504	0.501	0	0	0	0.502	0.194	0.809	0	0	0	0.498	0.191	0.806
SL005256	Histone H1.2	P16403	3006	HIST1H1C	RFU		No	No	DE	0.663	0.735	0.624	0	0	0	0.663	0.509	0.817	0	0	0	0.337	0.183	0.491
SL005258	PLK-1	P53350	5347	PLK1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005261	TCPTP	P17706	5771	PTPN2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005263	RAP	P30533	4043	LRPAP1	RFU		No	No	DE	0.848	0.900	0.809	0	0	0	0.848	0.785	0.912	0	0	0	0.152	0.088	0.215
SL005308	PSME3	P61289	10197	PSME3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005352	FABPE	Q01469	2171	FABP5	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005358	prostatic binding prote	P30086	5037	PEBP1	RFU		No	No	AE	0.727	0.794	0.685	0.727	0.614	0.840	0	0	0	0	0	0	0.273	0.160	0.386
SL005361	Apo D	P05090	347	APOD	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005372	Sorting nexin 4	O95219	8723	SNX4	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.653	0.537	0.770	0.347	0.230	0.463
SL005392	Arylsulfatase A	P15289	410	ARSA	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005437	MEPE	Q9NQ76	56955	MEPE	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005488	SPARCL1	Q14515	8404	SPARCL1	RFU		No	No	AE	0.761	0.829	0.716	0.761	0.657	0.865	0	0	0	0	0	0	0.239	0.135	0.343
SL005491	OBCAM	Q14982	4978	OPCML	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005493	paraoxose 1	P27169	5444	PON1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005508	Carbonic anhydrase 9	Q16790	768	CA9	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.297	0.111	0.483	0.703	0.517	0.889
SL005572	Gelsolin	P06396	2934	GSN	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005574	Aminoacylase-1	Q03154	95	ACY1	RFU		No	No	DE	0.333	0.159	0.390	0	0	0	0.333	0.078	0.589	0	0	0	0.667	0.411	0.922
SL005575	Fucosyltransferase 3	P21217	2525	FUT3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005588	FER	P16591	2241	FER	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.610	0.482	0.738	0.390	0.262	0.518
SL005629	GK	Q9UJ70	55577	GK	RFU		No	No	AE	0.625	0.678	0.596	0.625	0.477	0.773	0	0	0	0	0	0	0.375	0.227	0.523
SL005630	PSA6	P60900	5687	PSMA6	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.530	0.382	0.677	0.470	0.323	0.618
SL005675	ATP synthase beta cha	P06576	506	ATP5B	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005679	TCTP	P13693	7178	TPT1	RFU		No	No	AE	0.785	0.847	0.741	0.785	0.695	0.874	0	0	0	0	0	0	0.215	0.126	0.305
SL005685	EF-1-beta	P24534	1933	EEF1B2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.435	0.269	0.600	0.565	0.400	0.731
SL005687	eIF-5A-1	P63241	1984	EIF5A	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.596	0.464	0.728	0.404	0.272	0.536
SL005694	Peroxiredoxin-6	P30041	9588	PRDX6	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.670	0.557	0.782	0.330	0.218	0.443
SL005703	Notch 1	P46531	4851	NOTCH1	RFU		No	No	AE	0.513	0.521	0.510	0.513	0.327	0.700	0	0	0	0	0	0	0.487	0.300	0.673
SL005725	GRB2-related adapter	O75791	9402	GRAP2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL005730	cGMP-stimulated PDE	O00408	5138	PDE2A	RFU		No	No	DE	0.265	-0.014	0.348	0	0	0	0.265	-0.007	0.536	0	0	0	0.735	0.464	1.007
SL005764	sCD163	Q86VB7	9332	CD163	RFU		No	No	AE	0.723	0.786	0.683	0.723	0.613	0.833	0	0	0	0	0	0	0.277	0.167	0.387
SL005789	Stanniocalcin-1	P52823	6781	STC1	RFU		No	No	AE	0.688	0.753	0.650	0.688	0.560	0.817	0	0	0	0	0	0	0.312	0.183	0.440
SL005793	Cyclophilin F	P30405	10105	PPIF	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.584	0.450	0.718	0.416	0.282	0.550
SL005797	PIGR	P01833	5284	PIGR	RFU		No	No	AE	0.608	0.655	0.583	0.608	0.457	0.759	0	0	0	0	0	0	0.392	0.241	0.543
SL005846	Moesin	P26038	4478	MSN	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006029	Chitotriosidase-1	Q13231	1118	CHIT1	RFU		No	No	ACE	0.557	0.904	0.518	0.557	0.182	0.931	0	0	0	0.339	-0.038	0.716	0.104	0.057	0.151
SL006088	Sphingosine kise 1	Q9NYA1	8877	SPHK1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.699	0.594	0.803	0.301	0.197	0.406
SL006091	NCK1	P16333	4690	NCK1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006108	CD5L	O43866	922	CD5L	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.424	0.257	0.592	0.576	0.408	0.743
SL006114	ROR1	Q01973	4919	ROR1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1

SL006119	TFF3	Q07654	7033	TFF3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.184	-0.015	0.383	0.816	0.617	1.015
SL006132	Lamin-B1	P20700	4001	LMNB1	RFU		No	No	DE	0.546	0.599	0.530	0	0	0	0.546	0.278	0.814	0	0	0	0.454	0.186	0.722
SL006189	KIF23	Q02241	9493	KIF23	RFU		No	No	DE	0.362	0.171	0.413	0	0	0	0.362	0.071	0.654	0	0	0	0.638	0.346	0.929
SL006197	DJ homolog	Q96DA6	131118	DJC19	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006268	NSF1C	Q9UNZ2	55968	NSFL1C	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.479	0.321	0.636	0.521	0.364	0.679
SL006372	YES	P07947	7525	YES1	RFU		No	No	AE	0.704	0.770	0.664	0.704	0.581	0.826	0	0	0	0	0	0	0.296	0.174	0.419
SL006374	BMX	P51813	660	BMX	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006378	Esterase D	P10768	2098	ESD	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.337	0.155	0.519	0.663	0.481	0.845
SL006397	NRP1	O14786	8829	NRP1	RFU		No	No	AE	0.335	0.217	0.383	0.335	0.127	0.543	0	0	0	0	0	0	0.665	0.457	0.873
SL006406	PLXC1	O60486	10154	PLXNC1	RFU		No	No	AE	0.692	0.759	0.653	0.692	0.564	0.821	0	0	0	0	0	0	0.308	0.179	0.436
SL006448	HRG	P04196	3273	HRG	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.467	0.306	0.627	0.533	0.373	0.694
SL006460	GP1BA	P07359	2811	GP1BA	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006476	NMT1	P30419	4836	NMT1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.540	0.396	0.685	0.460	0.315	0.604
SL006480	TRY3	P35030	5646	PRSS3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006512	HGFA	Q04756	3083	HGFAC	RFU		No	No	AE	0.826	0.881	0.785	0.826	0.755	0.898	0	0	0	0	0	0	0.174	0.102	0.245
SL006522	LG3BP	Q08380	3959	LGALS3BP	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.739	0.646	0.832	0.261	0.168	0.354
SL006523	MFGM	Q08431	4240	MFGE8	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.494	0.340	0.649	0.506	0.351	0.660
SL006528	SEPR	Q12884	2191	FAP	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.255	0.061	0.450	0.745	0.550	0.939
SL006542	FCN2	Q15485	2220	FCN2	RFU		No	No	DE	0.707	0.788	0.662	0	0	0	0.707	0.567	0.848	0	0	0	0.293	0.152	0.433
SL006544	BGH3	Q15582	7045	TGFBI	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.385	0.208	0.563	0.615	0.437	0.792
SL006550	ECM1	Q16610	1893	ECM1	RFU		No	No	AE	0.493	0.487	0.495	0.493	0.285	0.700	0	0	0	0	0	0	0.507	0.300	0.715
SL006610	ATS13	Q76LX8	11093	ADAMTS13	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.600	0.468	0.732	0.400	0.268	0.532
SL006629	SIRT2	Q8IXJ6	22933	SIRT2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.431	0.265	0.598	0.569	0.402	0.735
SL006675	CKAP2	Q8WWK9	26586	CKAP2	RFU		No	No	AE	0.286	0.110	0.353	0.286	0.060	0.512	0	0	0	0	0	0	0.714	0.488	0.940
SL006694	CNDP1	Q96KN2	84735	CNDP1	RFU		No	No	AE	0.670	0.730	0.635	0.670	0.540	0.801	0	0	0	0	0	0	0.330	0.199	0.460
SL006698	transcription factor MLI	Q8N3X6	254251	LCORL	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006705	PFD5	Q99471	5204	PFDN5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.341	0.154	0.528	0.659	0.472	0.846
SL006713	Collectin Kidney 1	Q9BWP8	78989	COLEC11	RFU		No	No	AE	0.621	0.670	0.594	0.621	0.476	0.765	0	0	0	0	0	0	0.379	0.235	0.524
SL006777	FETUB	Q9UGM5	26998	FETUB	RFU		No	No	AE	0.638	0.690	0.609	0.638	0.502	0.775	0	0	0	0	0	0	0.362	0.225	0.498
SL006803	ANGL3	Q9Y5C1	27329	ANGPTL3	RFU		No	No	DE	0.919	0.955	0.887	0	0	0	0.919	0.878	0.959	0	0	0	0.081	0.041	0.122
SL006805	MRCKB	Q9Y5S2	9578	CDC42BPB	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006830	complement factor H-r	Q9BXR6	81494	CFHR5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.385	0.210	0.560	0.615	0.440	0.790
SL006892	ABL1	P00519	25	ABL1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006910	Cathepsin V	O60911	1515	CTSL2	RFU		No	No	AE	0.361	0.269	0.400	0.361	0.162	0.559	0	0	0	0	0	0	0.639	0.441	0.838
SL006911	CHK1	O14757	1111	CHEK1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006912	FGR	P09769	2268	FGR	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006913	FYN	P06241	2534	FYN	RFU		No	No	AE	0.672	0.729	0.638	0.672	0.548	0.797	0	0	0	0	0	0	0.328	0.203	0.452
SL006914	Glucocorticoid recepto	P04150	2908	NR3C1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.363	0.185	0.540	0.637	0.460	0.815
SL006915	IL-27	Q8NEV9	Q1	246778	10	IL27 EBI3	RFU		No	No	AE	0.264	-0.018	0.347	0.264	-0.008	0.536	0	0	0	0	0.736	0.464	1.008
SL006916	LCK	P06239	3932	LCK	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006917	LYN	P07948	4067	LYN	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.587	0.454	0.720	0.413	0.280	0.546
SL006918	MK01	P28482	5594	MAPK1	RFU		No	No	ACE	0.426	0.230	0.440	0.426	0.030	0.821	0	0	0	0.364	-0.016	0.744	0.210	0.118	0.302
SL006919	RSK-like protein kise	O75582	9252	RPS6KA5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.543	0.398	0.687	0.457	0.313	0.602
SL006920	MAPK14	Q16539	1432	MAPK14	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.569	0.431	0.707	0.431	0.293	0.569
SL006921	PDK1	Q15118	5163	PDK1	RFU		No	No	DE	0.264	-0.014	0.347	0	0	0	0.264	-0.007	0.534	0	0	0	0.736	0.466	1.007
SL006922	RAD51	Q06609	5888	RAD51	RFU		No	No	AE	0.438	0.403	0.455	0.438	0.255	0.621	0	0	0	0	0	0	0.562	0.379	0.745
SL006923	TBP	P20226	6908	TBP	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006924	ART	O00253	181	AGRP	RFU		No	No	DE	0.505	0.509	0.504	0	0	0	0.505	0.308	0.702	0	0	0	0.495	0.298	0.692
SL006970	DLL1	O00548	28514	DLL1	RFU		No	No	AE	0.257	0.054	0.333	0.257	0.030	0.485	0	0	0	0	0	0	0.743	0.515	0.970
SL006992	MATN3	O15232	4148	MATN3	RFU		No	No	DE	0.553	0.613	0.535	0	0	0	0.553	0.287	0.819	0	0	0	0.447	0.181	0.713
SL006993	MK13	O15264	5603	MAPK13	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL006998	PDPK1	O15530	5170	PDPK1	RFU		No	No	AE	0.730	0.794	0.689	0.730	0.622	0.838	0	0	0	0	0	0	0.270	0.162	0.378
SL007003	DHH	O43323	50846	DHH	RFU		No	No	AE	0.604	0.649	0.579	0.604	0.452	0.756	0	0	0	0	0	0	0.396	0.244	0.548
SL007022	HNRPQ	O60506	10492	SYNCRIP	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.259	0.063	0.456	0.741	0.544	0.937
SL007024	GREM1	O60565	26585	GREM1	RFU		No	No	AE	0.628	0.700	0.594	0.628	0.448	0.808	0	0	0	0	0	0	0.372	0.192	0.552
SL007025	JAK2	O60674	3717	JAK2	RFU		No	No	AE	0.779	0.841	0.736	0.779	0.687	0.870	0	0	0	0	0	0	0.221	0.130	0.313
SL007049	CYTF	O76096	8530	CST7	RFU		No	No	DE	0.721	0.784	0.681	0	0	0	0.721	0.610	0.832	0	0	0	0.279	0.168	0.390
SL007056	BMP10	O95393	27302	BMP10	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.240	0.046	0.434	0.760	0.566	0.954
SL007059	LY86	O95711	9450	LY86	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.211	0.010	0.411	0.789	0.589	0.990
SL007100	LKHA4	P09960	4048	LTA4H	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.506	0.354	0.658	0.494	0.342	0.646
SL007121	CATE	P14091	1510	CTSE	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007122	IDE	P14735	3416	IDE	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.182	-0.016	0.379	0.818	0.621	1.016
SL007145	NR1D1	P20393	9572	NR1D1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007153	PERL	P22079	4025	LPO	RFU		No	No	AE	0.550	0.579	0.537	0.550	0.366	0.734	0	0	0	0	0	0	0.450	0.266	0.634
SL007173	GRN	P28799	2896	GRN	RFU		No	No	DE	0.707	0.772	0.667	0	0	0	0.707	0.588	0.826	0	0	0	0.293	0.174	0.412
SL007179	EPHB2	P29323	2048	EPHB2	RFU		No	No	AE	0.533	0.549	0.525	0.533	0.371	0.695	0	0	0	0	0	0	0.467	0.305	0.629
SL007181	TYK2	P29597	7297	TYK2	RFU		No	No	AE	0.246	0.021	0.327	0.246	0.011	0.481	0	0	0	0	0	0	0.754	0.519	0.989
SL007195	CD70	P32970	970	CD70	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007206	TSP2	P35442	7058	THBS2	RFU		No	No	AE	0.496	0.493	0.497	0.496	0.306	0.686	0	0	0	0	0	0	0.504	0.314	0.694
SL007207	TSP4	P35443	7060	THBS4	RFU		No	No	AE	0.350	0.239	0.395	0.350	0.137	0.564	0	0	0	0	0	0	0.650	0.436	0.863
SL007228	KPCI	P41743	5584	PRKCI	RFU		No	No	AE	0.756	0.821	0.713	0.756	0.655	0.857	0	0	0	0	0	0	0.244	0.143	0.345
SL007237	MP2K4	P45985	6416	MAP2K4	RFU		No	No	ACE	0.365	-0.420	0.407	0.365	-0.042	0.772	0	0	0	0.375	-0.001	0.750	0.261	0.145	0.376
SL007250	PK3CG	P48736	5294	PIK3CG	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007261	AMPM2	P50579	10988	METAP2	RFU		No	No	AE	0.795	0.858	0.750	0.795	0.706	0.883	0	0	0	0	0	0	0.205	0.117	0.294
SL007266	PSD7	P51665	5713	PSMD7	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007280	CATC	P53634	1075	CTSC	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007281	MK12	P53778	6300	MAPK12	RFU		No	No	DE	0.678	0.759	0.635	0	0	0	0.678	0.521	0.834	0	0	0	0.322	0.166	0.479
SL007284	CRIS3	P54108	10321	CRISP3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007295	CAD15	P55291	1013	CDH15	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007324	CSK21	P68400	1457	CSNK2A1	RFU		No	No	DE	0.479	0.452	0.487	0	0	0	0.479	0.193	0.766	0	0	0	0.521	0.234	0.807
SL007327	OLR1	P78380	4973	OLR1	RFU		No	No	AE	0.403	0.329	0.432	0.403	0.187	0.618	0	0	0	0	0	0	0.597	0.382	0.813
SL007328	JAG1	P78504	182	JAG1	RFU		No	No	DE	0.651	0.714	0.617	0	0	0	0.651	0.505	0.798	0	0	0	0.349	0.202	0.495
SL007336	SET	Q01105	6418	SET	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.169	-0.040	0.378	0.831	0.622	1.040
SL007356	NOTC2	Q04721	4853	NOTCH2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007358	KPCT	Q04759	5588	PRKCQ	RFU		No	No	DE	0.243	-0.193	0.342	0	0	0	0.243	-0.072	0.557	0	0	0	0.757	0.443	1.072
SL007373	PPID	Q08752	5481	PPID	RFU		No	No	AE	0.747	0.812	0.704	0.747	0.643	0.852	0	0	0	0	0	0	0.253	0.148	0.357
SL007385	IL24	Q13007	11009	IL24	RFU		No	No	DE	0.200	-0.093	0.299	0	0	0	0.200	-0.047	0.448	0	0	0	0.800	0.552	1.047
SL007403	DMP1	Q13316	1758	DMP1	RFU		No	No	DE	0.236	-0.017	0.323	0	0	0	0.236	-0.009	0.480	0	0	0	0.764	0.520	1.009
SL007423	IL-11 RA	Q14626	3590	IL11RA	RFU		No	No	AE	0.211	-0.008	0.298	0.211	-0.005	0.427	0	0	0	0	0	0	0.789	0.573	1.005
SL007429	GPNMB	Q14956	10457	GPNMB	RFU		No	No	AE	0.678	0.737	0.642	0.678	0.552	0.803	0	0	0	0	0	0	0.322	0.197	0.448
SL007453	MK11	Q15759	5600	MAPK11	RFU		No	No	AE	0.187	-0.086	0.287	0.187	-0.046	0.420	0	0	0	0	0	0	0.813	0.580	1.046
SL007464	AMHR2	Q16671	269	AMHR2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.366	0.184	0.547	0.634	0.453	0.816
SL007471	COLEC12	Q5KU26	81035	COLEC12	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1

SL007502	ST4S6	Q7LFX5	51363	CHST15	RFU			No	No	AE	0.617	0.674	0.588	0.617	0.452	0.782	0	0	0	0	0	0	0.383	0.218	0.548
SL007531	BMPER	Q8N8U9	168667	BMPER	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007547	TIMD3	Q8TDQ0	84868	HAVCR2	RFU			No	No	AE	0.422	0.371	0.444	0.422	0.226	0.618	0	0	0	0	0	0	0.578	0.382	0.774
SL007560	STAB2	Q8WWQ8	55576	STAB2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007620	IL-12 RB2	Q99665	3595	IL12RB2	RFU			No	No	DE	0.315	0.136	0.376	0	0	0	0.315	0.069	0.560	0	0	0	0.685	0.440	0.931
SL007640	CLC7A	Q9BXN2	64581	CLEC7A	RFU			No	No	AE	0.707	0.786	0.663	0.707	0.570	0.845	0	0	0	0	0	0	0.293	0.155	0.430
SL007642	ANGL4	Q9BY76	51129	ANGPTL4	RFU			No	No	DE	0.335	0.098	0.396	0	0	0	0.335	0.040	0.629	0	0	0	0.665	0.371	0.960
SL007651	FGF23	Q9GZV9	8074	FGF23	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007673	NET4	Q9HB63	59277	NTN4	RFU			No	No	DE	0.440	0.390	0.459	0	0	0	0.440	0.213	0.667	0	0	0	0.560	0.333	0.787
SL007674	LY9	Q9HBG7	4063	LY9	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.541	0.397	0.686	0.459	0.314	0.603
SL007680	ROBO2	Q9HCK4	6092	ROBO2	RFU			No	No	AE	0.505	0.508	0.504	0.505	0.314	0.696	0	0	0	0	0	0	0.495	0.304	0.686
SL007729	ARTS1	Q9NZ08	51752	ERAP1	RFU			No	No	AE	0.724	0.796	0.681	0.724	0.603	0.846	0	0	0	0	0	0	0.276	0.154	0.397
SL007747	TBK1	Q9UHD2	29110	TBK1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.294	0.106	0.482	0.706	0.518	0.894
SL007752	DAPK2	Q9UIK4	23604	DAPK2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007756	GDF2	Q9UK05	2658	GDF2	RFU			No	No	DE	0.675	0.740	0.638	0	0	0	0.675	0.539	0.811	0	0	0	0.325	0.189	0.461
SL007774	JAG2	Q9Y219	3714	JAG2	RFU			No	No	DE	0.718	0.825	0.664	0	0	0	0.718	0.553	0.883	0	0	0	0.282	0.117	0.447
SL007804	BGN	P21810	633	BGN	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.500	0.347	0.654	0.500	0.346	0.653
SL007806	IL22RA1	Q8N6P7	58985	IL22RA1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007869	PPIB	P23284	5479	PPIB	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL007871	Cytidylate kise	P30085	51727	CMPK1	RFU			No	No	AE	0.503	0.505	0.502	0.503	0.325	0.681	0	0	0	0	0	0	0.497	0.319	0.675
SL007888	Cystatin-S	P01036	1472	CST4	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008008	ARGI1	P05089	383	ARG1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008023	HPLN1	P10915	1404	HAPLN1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008039	AK1A1	P14550	10327	AKR1A1	RFU			No	No	AE	0.829	0.884	0.787	0.829	0.756	0.901	0	0	0	0	0	0	0.171	0.099	0.244
SL008059	RS3	P23396	6188	RPS3	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008063	PPAC	P24666	52	ACP1	RFU			No	No	AE	0.824	0.882	0.781	0.824	0.748	0.900	0	0	0	0	0	0	0.176	0.100	0.252
SL008072	CO8A1	P27658	1295	COL8A1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008085	3HIDH	P31937	11112	HIBADH	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008099	CAPG	P40121	822	CAPG	RFU			No	No	AE	0.759	0.820	0.718	0.759	0.665	0.854	0	0	0	0	0	0	0.241	0.146	0.335
SL008102	MDHC	P40925	4190	MDH1	RFU			No	No	DE	0.784	0.856	0.736	0	0	0	0.784	0.682	0.886	0	0	0	0.216	0.114	0.318
SL008122	DUS3	P51452	1845	DUSP3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.551	0.409	0.693	0.449	0.307	0.591
SL008143	UBE2N	P61088	7334	UBE2N	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.622	0.497	0.747	0.378	0.253	0.503
SL008157	UB2L3	P68036	7332	UBE2L3	RFU			No	No	AE	0.756	0.823	0.712	0.756	0.653	0.859	0	0	0	0	0	0	0.244	0.141	0.347
SL008176	PSME1	Q06323	5720	PSME1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.467	0.307	0.628	0.533	0.372	0.693
SL008177	C1QBP	Q07021	708	C1QBP	RFU			No	No	DE	0.360	0.251	0.403	0	0	0	0.360	0.141	0.579	0	0	0	0.640	0.421	0.859
SL008178	DERM	Q07507	1805	DPT	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.437	0.269	0.604	0.563	0.396	0.731
SL008190	SPTA2	Q13813	6709	SPTAN1	RFU			No	No	DE	0.479	0.434	0.488	0	0	0	0.479	0.137	0.822	0	0	0	0.521	0.178	0.863
SL008193	NID2	Q14112	22795	NID2	RFU			No	No	AE	0.249	0.016	0.331	0.249	0.008	0.490	0	0	0	0	0	0	0.751	0.510	0.992
SL008309	RTN4	Q9NQC3	57142	RTN4	RFU			No	No	DE	0.572	0.607	0.555	0	0	0	0.572	0.410	0.735	0	0	0	0.428	0.265	0.590
SL008331	PA2G4	Q9UQ80	5036	PA2G4	RFU			No	No	AE	0.719	0.783	0.678	0.719	0.605	0.832	0	0	0	0	0	0	0.281	0.168	0.395
SL008378	4EBP2	Q13542	1979	EIF4EBP2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008380	CATZ	Q9UBR2	1522	CTSZ	RFU			No	No	AE	0.797	0.863	0.752	0.797	0.707	0.888	0	0	0	0	0	0	0.203	0.112	0.293
SL008382	CYTD	P28325	1473	CST5	RFU			No	No	AE	0.605	0.649	0.581	0.605	0.458	0.753	0	0	0	0	0	0	0.395	0.247	0.542
SL008414	EphB6	O15197	2051	EPHB6	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.205	0.003	0.406	0.795	0.594	0.997
SL008416	MRC2	Q9UBG0	9902	MRC2	RFU			No	No	DE	0.516	0.523	0.512	0	0	0	0.516	0.349	0.682	0	0	0	0.484	0.318	0.651
SL008421	ATS1	Q9UHI8	9510	ADAMTS1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008504	GNS	P15586	2799	GNS	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.163	-0.036	0.362	0.837	0.638	1.036
SL008516	CYTT	P09228	1470	CST2	RFU			No	No	AE	0.639	0.698	0.607	0.639	0.491	0.787	0	0	0	0	0	0	0.361	0.213	0.509
SL008574	OMD	Q99983	4958	OMD	RFU			No	No	DE	0.594	0.638	0.572	0	0	0	0.594	0.437	0.752	0	0	0	0.406	0.248	0.563
SL008588	SLAF5	Q9UIB8	8832	CD84	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.409	0.235	0.583	0.591	0.417	0.765
SL008590	Olfactomedin-4	Q6UX06	10562	OLFM4	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008611	ASAHL	Q02083	27163	AA	RFU			No	No	DE	0.654	0.719	0.619	0	0	0	0.654	0.506	0.802	0	0	0	0.346	0.198	0.494
SL008623	CNTN2	Q02246	6900	CNTN2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.520	0.371	0.670	0.480	0.330	0.629
SL008639	IDS	P22304	3423	IDS	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.440	0.275	0.605	0.560	0.395	0.725
SL008644	BST1	Q10588	683	BST1	RFU			No	No	AE	0.887	0.931	0.852	0.887	0.837	0.938	0	0	0	0	0	0	0.113	0.062	0.163
SL008703	CBPE	P16870	1363	CPE	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.340	0.158	0.522	0.660	0.478	0.842
SL008709	DSC3	Q14574	1825	DSC3	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008728	NRX3B	Q9HDB5	9369	NRXN3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.543	0.397	0.689	0.457	0.311	0.603
SL008759	GPVI	Q9HCN6	51206	GP6	RFU			No	No	DCE	0.271	-0.030	0.334	0	0	0	0.271	-0.010	0.552	0.467	0.209	0.725	0.262	0.146	0.377
SL008773	CD109	Q6YHK3	135228	CD109	RFU			No	No	AE	0.441	0.401	0.458	0.441	0.240	0.642	0	0	0	0	0	0	0.559	0.358	0.760
SL008808	SKP1	P63208	6500	SKP1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.624	0.499	0.749	0.376	0.251	0.501
SL008822	EMR2	Q9UHX3	30817	EMR2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.385	0.211	0.559	0.615	0.441	0.789
SL008835	ASGR1	P07306	432	ASGR1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008865	PSA2	P25787	5683	PSMA2	RFU			No	No	DE	0.493	0.488	0.495	0	0	0	0.493	0.291	0.695	0	0	0	0.507	0.305	0.709
SL008904	LYVE1	Q9Y5Y7	10894	LYVE1	RFU			No	No	DE	0.547	0.575	0.534	0	0	0	0.547	0.360	0.733	0	0	0	0.453	0.267	0.640
SL008909	LGMN	Q99538	5641	LGMN	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008916	DPP2	Q9UHL4	29952	DPP7	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008933	PARK7	Q99497	11315	PARK7	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL008936	CHL1	O00533	10752	CHL1	RFU			No	No	AE	0.556	0.584	0.542	0.556	0.387	0.725	0	0	0	0	0	0	0.444	0.275	0.613
SL008945	TGM3	Q08188	7053	TGM3	RFU			No	No	DE	0.498	0.496	0.498	0	0	0	0.498	0.319	0.676	0	0	0	0.502	0.324	0.681
SL008956	ARSB	P15848	411	ARSB	RFU			No	No	DE	0.717	0.810	0.667	0	0	0	0.717	0.568	0.867	0	0	0	0.283	0.133	0.432
SL009045	ENPP7	Q6UWV6	339221	ENPP7	RFU			No	No	DE	0.737	0.806	0.694	0	0	0	0.737	0.625	0.850	0	0	0	0.263	0.150	0.375
SL009054	NRX1B	P58400	9378	NRXN1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009089	PGCB	Q96GW7	63827	BCAN	RFU			No	No	DE	0.652	0.713	0.618	0	0	0	0.652	0.508	0.796	0	0	0	0.348	0.204	0.492
SL009202	JAML1	Q86YT9	120425	AMICA1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009207	Dyctin subunit 2	Q13561	10540	DCTN2	RFU			No	No	AE	0.272	0.076	0.344	0.272	0.041	0.504	0	0	0	0	0	0	0.728	0.496	0.959
SL009213	Cathepsin A	P10619	5476	CTSA	RFU			No	No	DE	0.460	0.430	0.472	0	0	0	0.460	0.245	0.675	0	0	0	0.540	0.325	0.755
SL009216	dopa decarboxylase	P20711	1644	DDC	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009324	FSTL3	O95633	10272	FSTL3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.603	0.471	0.735	0.397	0.265	0.529
SL009341	BASI	P35613	682	BSG	RFU			No	No	DE	0.293	0.000	0.370	0	0	0	0.293	0.000	0.586	0	0	0	0.707	0.414	1.000
SL009400	CRDL1	Q9BU40	91851	CHRDL1	RFU			No	No	AE	0.367	0.270	0.406	0.367	0.156	0.578	0	0	0	0	0	0	0.633	0.422	0.844
SL009412	DKK3	Q9UBP4	27122	DKK3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.280	0.087	0.474	0.720	0.526	0.913
SL009431	HINT1	P49773	3094	HINT1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009628	ING1	Q9UK53	3621	ING1	RFU			No	No	ACE	0.374	0.085	0.409	0.374	0.019	0.729	0	0	0	0.438	0.095	0.781	0.188	0.105	0.272
SL009629	MBD4	O95243	8930	MBD4	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009768	CBX5	P45973	23468	CBX5	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009790	RUXF	P62306	6636	SNRPF	RFU			No	No	AE	0.542	0.568	0.530	0.542	0.350	0.734	0	0	0	0	0	0	0.458	0.266	0.650
SL009791	hnRNP A/B	Q99729	3182	HNRNPAB	RFU			No	No	DE	0.665	0.737	0.626	0	0	0	0.665	0.513	0.817	0	0	0	0.335	0.183	0.487
SL009792	PUR8	P30566	158	ADSL	RFU	Calibration Scale		No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL009868	SSRP1	Q08945	6749	SSRP1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009951	WNT7A	O00755	7476	WNT7A	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL009988	ADAM12	O43184	8038	ADAM12	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010250	Stress-induced-phospl	P31948	10963	STIP1	RFU			No	No	AE	0.684	0.750	0.646	0.684	0.553	0.816	0	0	0	0	0	0	0.316	0.184	0.447

SL010288	Carbonic anhydrase 6	P23280	765	CA6	RFU	Calibration Scale		No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL010328	MED-1	Q15648	5469	MED1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010348	FN1.4	P02751	2335	FN1	RFU			No	No	DE	0.557	0.586	0.542	0	0	0	0.557	0.385	0.728	0	0	0	0.443	0.272	0.615
SL010349	FN1.3	P02751	2335	FN1	RFU			No	No	DE	0.734	0.804	0.691	0	0	0	0.734	0.619	0.849	0	0	0	0.266	0.151	0.381
SL010368	IDUA	P35475	3425	IDUA	RFU			No	No	DE	0.722	0.793	0.678	0	0	0	0.722	0.599	0.844	0	0	0	0.278	0.156	0.401
SL010369	Carbonic Anhydrase I	P22748	762	CA4	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.189	-0.010	0.387	0.811	0.613	1.010
SL010371	CD39	P49961	953	ENTPD1	RFU			No	No	DE	0.536	0.582	0.523	0	0	0	0.536	0.256	0.816	0	0	0	0.464	0.184	0.744
SL010372	Enterokise	P98073	5651	PRSS7	RFU			No	No	DE	0.714	0.836	0.657	0	0	0	0.714	0.532	0.896	0	0	0	0.286	0.104	0.468
SL010373	FCAR	P24071	2204	FCAR	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010374	METAP1	P53582	23173	METAP1	RFU			No	No	AE	0.742	0.816	0.696	0.742	0.625	0.860	0	0	0	0	0	0	0.258	0.140	0.375
SL010375	ASAH2	Q9NR71	56624	ASAH2	RFU			No	No	DE	0.697	0.763	0.658	0	0	0	0.697	0.572	0.822	0	0	0	0.303	0.178	0.428
SL010376	MMEL2	Q495T6	79258	MMEL1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010378	RET	P07949	5979	RET	RFU			No	No	AE	0.571	0.606	0.553	0.571	0.407	0.735	0	0	0	0	0	0	0.429	0.265	0.593
SL010379	Semaphorin 3A	Q14563	10371	SEMA3A	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010381	Soggy-1	Q9UK85	27120	DKKL1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.407	0.235	0.579	0.593	0.421	0.765
SL010384	Testican-1	Q08629	6695	SPOCK1	RFU			No	No	AE	0.709	0.780	0.667	0.709	0.584	0.835	0	0	0	0	0	0	0.291	0.165	0.416
SL010388	Trypsin 2	P07478	5645	PRSS2	RFU			No	No	AE	0.562	0.598	0.546	0.562	0.379	0.746	0	0	0	0	0	0	0.438	0.254	0.621
SL010390	URB	Q76M96	151887	CCDC80	RFU			No	No	DE	0.505	0.508	0.504	0	0	0	0.505	0.327	0.683	0	0	0	0.495	0.317	0.673
SL010391	WFKN2	Q8TEU8	124857	WFIKKN2	RFU			No	No	AE	0.595	0.638	0.573	0.595	0.441	0.749	0	0	0	0	0	0	0.405	0.251	0.559
SL010392	GASP-2	Q96D09	114928	GPRASP2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.222	0.028	0.417	0.778	0.583	0.972
SL010393	KREM2	Q8NCW0	79412	KREMEN2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010449	Carbonic Anhydrase X	Q9NS85	56934	CA10	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010450	CD48	P09326	962	CD48	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.296	0.105	0.486	0.704	0.514	0.895
SL010451	CFC1	P0CG37	55997	CFC1	RFU			No	No	DE	0.342	0.221	0.390	0	0	0	0.342	0.125	0.560	0	0	0	0.658	0.440	0.875
SL010454	Contactin-4	Q8IWV2	152330	CNTN4	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.544	0.396	0.693	0.456	0.307	0.604
SL010455	Contactin-5	O94779	53942	CNTN5	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010456	CYTN	P01037	1469	CST1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.283	0.096	0.471	0.717	0.529	0.904
SL010457	DLL4	Q9NR61	54567	DLL4	RFU			No	No	DE	0.338	-0.031	0.405	0	0	0	0.338	-0.010	0.686	0	0	0	0.662	0.314	1.010
SL010458	Endocan	Q9NQ30	11082	ESM1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010461	FCGR1	P12314	2209	FCGR1A	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010462	FCN1	O00602	2219	FCN1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010463	GPC2	Q8N158	221914	GPC2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.261	0.070	0.451	0.739	0.549	0.930
SL010464	LRIG3	Q6UXM1	121227	LRIG3	RFU			No	No	AE	0.514	0.522	0.510	0.514	0.330	0.698	0	0	0	0	0	0	0.486	0.302	0.670
SL010465	MATN2	O00339	4147	MATN2	RFU			No	No	AE	0.470	0.452	0.479	0.470	0.278	0.663	0	0	0	0	0	0	0.530	0.337	0.722
SL010466	MFRP	Q9BY79	83552	MFRP	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.255	0.064	0.446	0.745	0.554	0.936
SL010467	RGMA	Q96B86	56963	RGMA	RFU			No	No	AE	0.440	0.396	0.458	0.440	0.227	0.653	0	0	0	0	0	0	0.560	0.347	0.773
SL010468	RGMB	Q6NW40	285704	RGMB	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.275	0.076	0.474	0.725	0.526	0.924
SL010469	RGM-C	Q6ZVN8	148738	HFE2	RFU			No	No	AE	0.455	0.424	0.468	0.455	0.249	0.662	0	0	0	0	0	0	0.545	0.338	0.751
SL010470	Semaphorin 3E	O15041	9723	SEMA3E	RFU			No	No	AE	0.630	0.683	0.601	0.630	0.485	0.775	0	0	0	0	0	0	0.370	0.225	0.515
SL010471	Testican-2	Q92563	9806	SPOCK2	RFU			No	No	AE	0.699	0.761	0.661	0.699	0.581	0.817	0	0	0	0	0	0	0.301	0.183	0.419
SL010488	ABL2	P42684	27	ABL2	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010489	CAMK1	Q14012	8536	CAMK1	RFU	Calibration Scale		No	No	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SL010490	CAMK1D	Q8IU85	57118	CAMK1D	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.214	0.016	0.412	0.786	0.588	0.984
SL010491	CAMK2A	Q9UQM7	815	CAMK2A	RFU			No	No	AE	0.699	0.763	0.660	0.699	0.577	0.821	0	0	0	0	0	0	0.301	0.179	0.423
SL010492	CAMK2B	Q13554	816	CAMK2B	RFU			No	No	DE	0.368	0.242	0.411	0	0	0	0.368	0.124	0.612	0	0	0	0.632	0.388	0.876
SL010493	CAMK2D	Q13557	817	CAMK2D	RFU			No	No	AE	0.769	0.835	0.725	0.769	0.671	0.867	0	0	0	0	0	0	0.231	0.133	0.329
SL010494	CDK1/cyclin B	P06493 P14	983 891	CDC2 CCNB1	RFU			No	No	DE	0.870	0.926	0.827	0	0	0	0.870	0.805	0.936	0	0	0	0.130	0.064	0.195
SL010495	CDK2/cyclin A	P24941 P20	1017 890	CDK2 CC2	RFU			No	No	DE	0.267	0.000	0.348	0	0	0	0.267	0.000	0.534	0	0	0	0.733	0.466	1.000
SL010496	CDK5/p35	Q00535 Q1	1020 8851	CDK5 CDK5R1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010498	EPHA3	P29320	2042	EPHA3	RFU			No	No	AE	0.604	0.667	0.575	0.604	0.414	0.794	0	0	0	0	0	0	0.396	0.206	0.586
SL010499	HCK	P08631	3055	HCK	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.216	0.019	0.414	0.784	0.586	0.981
SL010500	LYNB	P07948	4067	LYN	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.515	0.366	0.665	0.485	0.335	0.634
SL010501	MP2K2	P36507	5605	MAP2K2	RFU			No	No	DE	0.786	0.850	0.742	0	0	0	0.786	0.695	0.878	0	0	0	0.214	0.122	0.305
SL010502	MK08	P45983	5599	MAPK8	RFU			No	No	DE	0.621	0.689	0.589	0	0	0	0.621	0.443	0.800	0	0	0	0.379	0.200	0.557
SL010503	MAPK2	P49137	9261	MAPKAPK2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.471	0.313	0.630	0.529	0.370	0.687
SL010504	MAPK5	Q8IW41	8550	MAPKAPK5	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010505	MATK	P42679	4145	MATK	RFU			No	No	DE	0.283	-0.133	0.369	0	0	0	0.283	-0.045	0.612	0	0	0	0.717	0.388	1.045
SL010508	PAK3	O75914	5063	PAK3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.168	-0.033	0.369	0.832	0.631	1.033
SL010509	PAK6	Q9NQU5	56924	PAK6	RFU			No	No	AE	0.760	0.824	0.717	0.760	0.661	0.859	0	0	0	0	0	0	0.240	0.141	0.339
SL010510	PAK7	Q9P286	57144	PAK7	RFU			No	No	AE	0.449	0.418	0.463	0.449	0.263	0.634	0	0	0	0	0	0	0.551	0.366	0.737
SL010512	PIK3CA/PIK3R1	P42336 P27	5290 5295	PIK3CA PIK3R1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010513	PRKACA	P17612	5566	PRKACA	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.553	0.412	0.695	0.447	0.305	0.588
SL010514	PTK6	Q13882	5753	PTK6	RFU			No	No	DE	0.381	0.241	0.422	0	0	0	0.381	0.111	0.650	0	0	0	0.619	0.350	0.889
SL010515	RPS6KA3	P51812	6197	RPS6KA3	RFU			No	No	DE	0.670	0.745	0.630	0	0	0	0.670	0.517	0.823	0	0	0	0.330	0.177	0.483
SL010516	SRCN1	P12931	6714	SRC	RFU			No	No	AE	0.718	0.782	0.677	0.718	0.604	0.832	0	0	0	0	0	0	0.282	0.168	0.396
SL010517	STK16	O75716	8576	STK16	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010518	TEC	P42680	7006	TEC	RFU			No	No	DE	0.546	0.573	0.533	0	0	0	0.546	0.356	0.735	0	0	0	0.454	0.265	0.644
SL010519	ZAP70	P43403	7535	ZAP70	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.426	0.256	0.595	0.574	0.405	0.744
SL010520	AURKB	Q96GD4	9212	AURKB	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.180	-0.023	0.383	0.820	0.617	1.023
SL010521	BTK	Q06187	695	BTK	RFU			No	No	ACE	0.394	-0.508	0.424	0.394	-0.032	0.820	0	0	0	0.349	-0.051	0.748	0.257	0.146	0.369
SL010522	CDK8/cyclin C	P49336 P24	1024 892	CDK8 CCNC	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.396	0.220	0.571	0.604	0.429	0.780
SL010523	HIPK3	Q9H422	10114	HIPK3	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.206	0.010	0.401	0.794	0.599	0.990
SL010528	UFM1	P61960	51569	UFM1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.445	0.281	0.609	0.555	0.391	0.719
SL010529	UFC1	Q9Y3C8	51506	UFC1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.490	0.334	0.645	0.510	0.355	0.666
SL010530	OCAD1	Q9NX40	54940	OCIAD1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010610	CLC4K	Q9UJ71	50489	CD207	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010612	Dkk-4	Q9UBT3	27121	DKK4	RFU			No	No	AE	0.540	0.564	0.530	0.540	0.357	0.724	0	0	0	0	0	0	0.460	0.276	0.643
SL010613	IL-17 RD	Q8NFM7	54756	IL17RD	RFU			No	No	DE	0.364	0.249	0.407	0	0	0	0.364	0.135	0.593	0	0	0	0.636	0.407	0.865
SL010616	SHP-2	Q06124	5781	PTPN11	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.527	0.379	0.675	0.473	0.325	0.621
SL010617	TPSB2	P20231	64499	TPSB2	RFU			No	No	ACE	0.635	1.021	0.569	0.635	0.294	0.975	0	0	0	0.304	-0.039	0.647	0.062	0.033	0.090
SL010619	TPSG1	Q9NRR2	25823	TPSG1	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL010830	41	P11171	2035	EPB41	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.479	0.321	0.636	0.521	0.364	0.679
SL010927	IMB1	Q14974	3837	KPNB1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.496	0.342	0.650	0.504	0.350	0.658
SL010928	IMDH2	P12268	3615	IMPDH2	RFU			No	No	DE	0.622	0.683	0.592	0	0	0	0.622	0.456	0.789	0	0	0	0.378	0.211	0.544
SL010973	PSA1	P25786	5682	PSMA1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.278	0.085	0.471	0.722	0.529	0.915
SL011049	MASP3	P48740	5648	MASP1	RFU			No	No	DE	0.564	0.597	0.548	0	0	0	0.564	0.397	0.732	0	0	0	0.436	0.268	0.603
SL011068	IL-17 RC	Q8C3	84818	IL17RC	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.193	-0.004	0.389	0.807	0.611	1.004
SL011069	Marapsin	Q9BQR3	83886	PRSS27	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.413	0.242	0.585	0.587	0.415	0.758
SL011071	PDGF-CC	Q9NRA1	56034	PDGFC	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011073	XPNPEP1	Q9NQW7	7511	XPNPEP1	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.479	0.322	0.636	0.521	0.364	0.678
SL011100	CD226	Q15762	10666	CD226	RFU			No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011202	SA	P54920	8775	PA	RFU			No	No	ACE	0.362	-0.133	0.404	0.362	-0.021	0.746	0	0	0	0.409	0.048	0.769	0.229	0.128	0.330
SL011211	IF4G2	P78344	1982	EIF4G2	RFU			No	No	CE	0	0	0	0	0	0	0	0	0	0.572	0.435	0.709	0.428	0.291	0.565

SL011232	CDC37	Q16543	11140	CDC37	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011404	PDE4D	Q08499	5144	PDE4D	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011405	PDE5A	O76074	8654	PDE5A	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.578	0.442	0.714	0.422	0.286	0.558
SL011406	PDE7A	Q13946	5150	PDE7A	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011448	TNR4	P43489	7293	TNFRSF4	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011498	PACAP-38	P18509	116	ADCYAP1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011499	PH	P01298	5539	PPY	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.398	0.227	0.570	0.602	0.430	0.773
SL011508	PACAP-27	P18509	116	ADCYAP1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011509	PYY	P10082	5697	PYY	RFU		No	No	AE	0.639	0.700	0.606	0.639	0.486	0.792	0	0	0	0	0	0	0.361	0.208	0.514
SL011510	Somatostatin-28	P61278	6750	SST	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011528	RS7	P62081	6201	RPS7	RFU		No	No	DE	0.522	0.537	0.516	0	0	0	0.522	0.320	0.725	0	0	0	0.478	0.275	0.680
SL011529	SBDS	Q9Y3A5	51119	SBDS	RFU		No	No	AE	0.730	0.792	0.689	0.730	0.623	0.837	0	0	0	0	0	0	0.270	0.163	0.377
SL011530	DLRB1	Q9NP97	83658	DYNLRB1	RFU		No	No	AE	0.722	0.784	0.683	0.722	0.613	0.831	0	0	0	0	0	0	0.278	0.169	0.387
SL011532	ETHE1	O95571	23474	ETHE1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.389	0.216	0.563	0.611	0.437	0.784
SL011533	SGTA	O43765	6449	SGTA	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.423	0.255	0.591	0.577	0.409	0.745
SL011535	RBM39	Q14498	9584	RBM39	RFU		No	No	DE	0.592	0.676	0.562	0	0	0	0.592	0.352	0.831	0	0	0	0.408	0.169	0.648
SL011549	ARI3A	Q99856	1820	ARID3A	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.261	0.070	0.451	0.739	0.549	0.930
SL011616	IF4A3	P38919	9775	EIF4A3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011628	DBNL	Q9UJU6	28988	DBNL	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.159	-0.040	0.359	0.841	0.641	1.040
SL011629	AIP	O00170	9049	AIP	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.609	0.480	0.738	0.391	0.262	0.520
SL011630	SE6L2	Q6UXD5	26470	SEZ6L2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.409	0.238	0.579	0.591	0.421	0.762
SL011631	CA	Q13765	4666	CA	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.451	0.289	0.614	0.549	0.386	0.711
SL011708	ARP19	P56211	10776	ARPP19	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.502	0.350	0.655	0.498	0.345	0.650
SL011709	PLPP	Q96GD0	57026	PDXP	RFU		No	No	AE	0.756	0.820	0.713	0.756	0.655	0.856	0	0	0	0	0	0	0.244	0.144	0.345
SL011768	NUDC3	Q8IVD9	23386	NUDCD3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.374	0.197	0.552	0.626	0.448	0.803
SL011769	AN32B	Q92688	10541	ANP32B	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.433	0.268	0.599	0.567	0.401	0.732
SL011770	LCMT1	Q9UIC8	51451	LCMT1	RFU		No	No	AE	0.484	0.470	0.489	0.484	0.261	0.707	0	0	0	0	0	0	0.516	0.293	0.739
SL011772	PESC	O00541	23481	PES1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL011808	CPNE1	Q99829	8904	CPNE1	RFU		No	No	AE	0.826	0.885	0.782	0.826	0.749	0.903	0	0	0	0	0	0	0.174	0.097	0.251
SL011809	XTP3A	Q9H773	79077	DCTPP1	RFU		No	No	AE	0.366	0.271	0.406	0.366	0.158	0.575	0	0	0	0	0	0	0.634	0.425	0.842
SL012108	PLCG1	P19174	5335	PLCG1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL012168	LIN7B	Q9HAP6	64130	LIN7B	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL012188	EP15R	Q9UBC2	58513	EPS15L1	RFU		No	No	AE	0.397	0.315	0.429	0.397	0.176	0.618	0	0	0	0	0	0	0.603	0.382	0.824
SL012248	FAK1	Q05397	5747	PTK2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL012457	NXPH1	P58417	30010	NXPH1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.732	0.637	0.827	0.268	0.173	0.363
SL012469	GPC5	P78333	2262	GPC5	RFU		No	No	AE	0.472	0.453	0.480	0.472	0.276	0.667	0	0	0	0	0	0	0.528	0.333	0.724
SL012538	ARMEL	Q49AH0	441549	CDNF	RFU		No	No	AE	0.319	0.178	0.374	0.319	0.100	0.538	0	0	0	0	0	0	0.681	0.462	0.900
SL012698	KI2L4	Q99706	3805	KIR2DL4	RFU		No	No	DE	0.218	-0.045	0.310	0	0	0	0.218	-0.023	0.459	0	0	0	0.782	0.541	1.023
SL012707	PCSK9	Q8NBP7	255738	PCSK9	RFU		No	No	DE	0.558	0.594	0.542	0	0	0	0.558	0.369	0.748	0	0	0	0.442	0.252	0.631
SL012740	ATS15	Q8TE58	170689	ADAMTS15	RFU		No	No	DE	0.480	0.451	0.488	0	0	0	0.480	0.184	0.777	0	0	0	0.520	0.223	0.816
SL012754	ASM3A	Q92484	10924	SMPDL3A	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.209	0.013	0.406	0.791	0.594	0.987
SL012822	BSSP4	Q9GZN4	64063	PRSS22	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.539	0.392	0.686	0.461	0.314	0.608
SL013240	CRK	P46108	1398	CRK	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.508	0.356	0.659	0.492	0.341	0.644
SL013488	CLC1B	Q9P126	51266	CLEC1B	RFU		No	No	AE	0.726	0.794	0.684	0.726	0.611	0.842	0	0	0	0	0	0	0.274	0.158	0.389
SL013489	AMNLS	Q9BXJ7	81693	AMN	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.277	0.087	0.467	0.723	0.533	0.913
SL013490	BOC	Q9BWV1	91653	BOC	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.171	-0.028	0.370	0.829	0.630	1.028
SL013548	IL-34	Q6ZMJ4	146433	IL34	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL013570	DYRK3	O43781	8444	DYRK3	RFU		No	No	DE	0.298	-0.061	0.377	0	0	0	0.298	-0.022	0.618	0	0	0	0.702	0.382	1.022
SL013754	RASA1	P20936	5921	RASA1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.149	-0.055	0.353	0.851	0.647	1.055
SL013928	PPIE	Q9UNP9	10450	PPIE	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.563	0.423	0.703	0.437	0.297	0.577
SL013969	KYNU	Q16719	8942	KYNU	RFU		No	No	DE	0.525	0.540	0.518	0	0	0	0.525	0.331	0.718	0	0	0	0.475	0.282	0.669
SL013988	CHST2	Q9Y4C5	9435	CHST2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.380	0.205	0.555	0.620	0.445	0.795
SL013989	RSPO2	Q6UXX9	340419	RSPO2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014008	FUT5	Q11128	2527	FUT5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.542	0.398	0.687	0.458	0.313	0.602
SL014009	HDGR2	Q7Z4V5	84717	HDGFRP2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014028	ENTP5	O75356	957	ENTPD5	RFU		No	No	AE	0.663	0.721	0.629	0.663	0.532	0.795	0	0	0	0	0	0	0.337	0.205	0.468
SL014029	SPHK2	Q9NRA0	56848	SPHK2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014048	CO1	Q86Y22	91522	COL23A1	RFU		No	No	DCE	0.274	0.041	0.333	0	0	0	0.274	0.017	0.532	0.512	0.266	0.757	0.214	0.120	0.309
SL014069	PCSK7	Q16549	9159	PCSK7	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.620	0.493	0.746	0.380	0.254	0.507
SL014070	SLIK5	O94991	26050	SLITRK5	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.374	0.198	0.550	0.626	0.450	0.802
SL014071	FLRT1	Q9NZU1	23769	FLRT1	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.392	0.218	0.566	0.608	0.434	0.782
SL014088	FCRL3	Q96P31	115352	FCRL3	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.228	0.033	0.422	0.772	0.578	0.967
SL014091	SORC2	Q96PQ0	57537	SORCS2	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014092	CDON	Q4KMG0	50937	CDON	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.468	0.306	0.630	0.532	0.370	0.694
SL014093	ENTP3	O75355	956	ENTPD3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014094	GP114	Q8IZF4	221188	GPR114	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014096	LRRT1	Q86UE6	347730	LRRTM1	RFU		No	No	DE	0.158	-0.104	0.262	0	0	0	0.158	-0.059	0.375	0	0	0	0.842	0.625	1.059
SL014108	LRRT3	Q86VH5	347731	LRRTM3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014111	KIRR3	Q8IZU9	84623	KIRREL3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014113	NLGNX	Q8N0W4	57502	NLGN4X	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.215	0.019	0.411	0.785	0.589	0.981
SL014129	H6ST1	O60243	9394	HS6ST1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014130	CHST6	Q9GZX3	4166	CHST6	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014148	ROBO3	Q96MS0	64221	ROBO3	RFU		No	No	DE	0.699	0.809	0.647	0	0	0	0.699	0.521	0.877	0	0	0	0.301	0.123	0.479
SL014208	CRTAM	O95727	56253	CRTAM	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014209	KLRF1	Q9NZS2	51348	KLRF1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014228	SLAF6	Q96DU3	114836	SLAMF6	RFU		No	No	DE	0.332	0.185	0.386	0	0	0	0.332	0.098	0.566	0	0	0	0.668	0.434	0.902
SL014268	OX2G	P41217	4345	CD200	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.308	0.122	0.494	0.692	0.506	0.878
SL014269	KI3L2	P43630	3812	KIR3DL2	RFU		No	No	DE	0.270	0.045	0.346	0	0	0	0.270	0.023	0.516	0	0	0	0.730	0.484	0.977
SL014270	CLM6	Q08708	10871	CD300C	RFU		No	No	AE	0.345	0.230	0.391	0.345	0.133	0.556	0	0	0	0	0	0	0.655	0.444	0.867
SL014288	MO2R1	Q8TD46	131450	CD200R1	RFU		No	No	DE	0.367	0.257	0.408	0	0	0	0.367	0.141	0.593	0	0	0	0.633	0.407	0.859
SL014289	KI3S1	Q14943	3813	KIR3DS1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014292	SIG14	Q08ET2	1E+08	SIGLEC14	RFU		No	No	DE	0.974	0.986	0.963	0	0	0	0.974	0.962	0.986	0	0	0	0.026	0.014	0.038
SL014294	EPHAA	Q5JZY3	284656	EPHA10	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014308	FGF-8A	P55075	2253	FGF8	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.167	-0.032	0.366	0.833	0.634	1.032
SL014468	SH21A	O60880	4068	SH2D1A	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.165	-0.034	0.364	0.835	0.636	1.034
SL014469	SHC1	P29353	6464	SHC1	RFU		No	No	AE	0.684	0.746	0.647	0.684	0.557	0.811	0	0	0	0	0	0	0.316	0.189	0.443
SL014470	BCAR3	O75815	8412	BCAR3	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL014735	IMDH1	P20839	3614	IMPDH1	RFU		No	No	AE	0.657	0.724	0.621	0.657	0.507	0.807	0	0	0	0	0	0	0.343	0.193	0.493
SL015728	GCKR	Q14397	2646	GCKR	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL016128	TXD12	O95881	51060	TXNDC12	RFU		No	No	AE	0.869	0.918	0.830	0.869	0.810	0.928	0	0	0	0	0	0	0.131	0.072	0.190
SL016129	FAM107B	Q9H098	83641	FAM107B	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.186	-0.012	0.384	0.814	0.616	1.012
SL016130	BRF-1	Q92994	2972	BRF1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL016148	C34 gp41 HIV Fragme	Q70626	None	Human-virus	RFU		No	No	DE	0.331	0.122	0.391	0	0	0	0.331	0.054	0.608	0	0	0	0.669	0.392	0.946

SL016548	AMPK a1b1g1	Q13131	Q9\	5562	5564	PRKAA1	PRKAB	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL016549	AMPK a2b2g1	P54646	O43	5563	5565	PRKAA2	PRKAB	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.181	-0.017	0.378	0.819	0.622	1.017
SL016550	CK2-A1:B	P68400	P67	1457	1460	CSNK2A1	CSNK	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.680	0.571	0.790	0.320	0.210	0.429
SL016551	CK2-A2:B	P19784	P67	1459	1460	CSNK2A2	CSNK	RFU		No	No	AE	0.208	-0.114	0.308	0.208	-0.054	0.470	0	0	0	0	0	0	0.792	0.530	1.054
SL016553	PDE3A	Q14432		5139		PDE3A		RFU		No	No	DE	0.501	0.502	0.501	0	0	0	0.501	0.289	0.713	0	0	0	0.499	0.287	0.711
SL016554	PDE9A	O76083		5152		PDE9A		RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL016555	PDE11	Q9HCR9		50940		PDE11A		RFU		No	No	DE	0.655	0.727	0.618	0	0	0	0.655	0.497	0.813	0	0	0	0.345	0.187	0.503
SL016557	HMGR	P04035		3156		HMGCR		RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL016563	GHC2	Q9H1K4		83733		SLC25A18		RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL016566	DRAK2	O94768		9262		STK17B		RFU		No	No	DE	0.710	0.788	0.665	0	0	0	0.710	0.575	0.845	0	0	0	0.290	0.155	0.425
SL016567	TAK1-TAB1	O43318	Q15	6885	10454	MAP3K7	TAB1	RFU		No	No	E	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
SL016928	SLAF7	Q9NQ25		57823		SLAMF7		RFU		No	No	AE	0.902	0.939	0.871	0.902	0.860	0.944	0	0	0	0	0	0	0.098	0.056	0.140
SL017188	GSK-3 alpha/beta	P49840	P49	2931	2932	GSK3A	GSK3B	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.649	0.531	0.767	0.351	0.233	0.469
SL017189	Kininogen HMW	P01042		3827		KNG1		RFU		No	No	AE	0.596	0.644	0.572	0.596	0.429	0.763	0	0	0	0	0	0	0.404	0.237	0.571
SL017610	Gro-b/g	P19876	P19	None		CXCL3	CXCL2	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.432	0.267	0.598	0.568	0.402	0.733
SL017611	14/03/2003	P31946	P62	7529	7531	YWHAB	YWHAE	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.626	0.502	0.750	0.374	0.250	0.498
SL017612	HSP 90a/b	P07900	P08	None		HSP90AA1	HSP	RFU		No	No	DCE	0.253	-0.049	0.321	0	0	0	0.253	-0.018	0.524	0.496	0.246	0.747	0.250	0.140	0.361
SL017613	FCG2A/B	P12318	P31	None		FCGR2A	FCGR2	RFU		No	No	DE	0.940	0.965	0.917	0	0	0	0.940	0.913	0.967	0	0	0	0.060	0.033	0.087
SL017614	PKB a/b/g	Family		None		None		RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.639	0.519	0.760	0.361	0.240	0.481
SL018625	TLR4:MD-2 complex	O00206	Q9	7099	23643	TLR4	LY96	RFU		No	No	CE	0	0	0	0	0	0	0	0	0	0.593	0.459	0.727	0.407	0.273	0.541